Sequence:

Run on:

Sequence 1, Appli Sequence 1, Appli Sequence 5551, Ap Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 128, Appli Sequence 1128, Appli Sequence 1138, Appli Sequence 1138, Appli Sequence 11, Appli Sequence 1058, Appli

Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli

Sequence 1, Appli Sequence 1899, Ap Sequence 1168, Ap

```
3 IlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp-SerSe 22 ::: ::: ::: ::: ||||||||::: ||| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.

PAPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Beed, Steven G.

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.475C1

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

RARLIER APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-04-02

MUMBER OF SEQ ID NOS: 289

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSEQ for Windows Version 3.0
              US-08-730-163-1

US-08-730-163-1

US-08-45-437-1

US-08-62-563A-5551

US-09-489-039A-5551

US-09-489-039A-5551

US-09-161-976-13459

US-09-161-976-13459

US-09-162-047-5

US-09-162-047-5

US-09-162-047-5

US-09-162-047-5

US-09-162-047-5

US-09-162-047-11285

US-09-162-047-11285

US-09-134-000C-1058

US-09-134-000C-1058

US-09-134-000C-1058

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-134-1168

US-09-144-5

US-09-144-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168

US-09-146-1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-10 (1-58) x US-09-370-838-66 (1-2581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
6.62
69.50
56.14%
35.09%
21.99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-370-838-66
                                                                                                                                                                                                                                                                                                                                                                  61.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66, Appl
Sequence 21, Appl
Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3819, Appli
Sequence 3819, Appli
Sequence 3819, Appli
Sequence 3819, Appli
                                                                                                                 August 15, 2004, 22:31:28 ; Search time 60 Seconds (without alignments) 536.453 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                             316
1 MKIFIFVFIMALILAMIRAD......QQXQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                     OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2581 4 US-09-370-838-66
3164 4 US-09-023-655-816
94401529 3 US-09-103-840A-2
6 2335 3 US-09-387-574-9
6 2335 4 US-09-568-096-9
6 2335 4 US-09-668-096-9
3 4379 1 US-08-562-214A-17
1 4403765 3 US-09-103-840A-1
1 4411529 3 US-09-1359-3319
9 750 4 US-09-359-301A-30
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                        US-10-079-754A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
65
64
64
63
63
63
                                                                                                                                                                                                                                                             Scoring table:
```

K400700111

Result No.

```
1164 AGAGGAGTCGCCGCCATCTTCAGAGGAGTCCCCATTCTCATCATCTTCCTCTTCTTCATC 1105
22 rGluGlu-LysArgHisArgLysArgLysLysHis---HisArgGlyTyrPheGlnGlnT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various positions throughout the sequence \boldsymbol{t} , \boldsymbol{c} or \boldsymbol{g}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09103840A

Patent No. 629423

GENEAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: WENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE PETCHING DATE: 1998-06-24
NUMBER: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHAM, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCLUCSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                          1104 CTCGTCCTCGTCATCCTCATCCTCTCATCATCCTCCTCGGACTCCG 1058
                                                                                                     41 yrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1189236 CACCACCGGTACCACCTTACCGGCGGTGGCCA 1189268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-10 (1-58) x US-09-103-840A-2 (1-4403765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at
CHER INFORMATION: represent a,
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 4411529
```

```
US-08-592-214A-17
                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                       2335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 CGGCACCGGCCTCCCGGAGTCCGTCCTCGCCGCCGCCGCCGCCGCCGGGAAGACGGT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 MetAlaLeulleLeuAlaMetIleArgAlaAspSerSerGluGluLysArgHisArgLys 29
                                                                                                                                                                    18 ArgalaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 -----GlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 cedarrecesesesasaseraceceacedaredacececacerestresassistes
                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09387574

Sequence 9, Application US/09387574

Sequence 9, Application US/09387574

Sequence 9, Application US/09387574

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: RafalsK1, Antoni
ITILE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REFERENCE: BB-1239
FILE REFERENCE: BB-1239

CURRENT APPLICATION NUMBER: US/09/387,574

CURRENT FILING DATE: September 1, 1998

SEQUENCE: Microsoft Office 97

SEQUENCE: Microsoft Office 97

FEMILIES MICROSOFT OFFICE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LysLysHisHisArgGlyTyrPhe-
                                                                                                                                                                                                                                               |||||||||:::||||
1189210 CACCACCCGTACCACCCTTACCGGCGGTGGCCA 1189242
                                                                                                                                           US-10-079-754A-10 (1-58) x US-09-103-840A-1 (1-4411529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-079-754A-10 (1-58) x US-09-387-574-9 (1-2335)
                                                                                                                                                                                                                                 38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
                                       5.07e+05
66.00
58.06%
32.26%
20.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.7
65.00
34.15%
25.61%
20.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
US-09-387-574-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 Arg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trecer 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phepro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2335
JS-09-103-840A-1
                                                                                                                                                                                                                                                                                             RESULT 5
US-09-387-574-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local S
Query Match:
                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                    ò
```

```
174 desarreceesesasarraceedalearedadeesesarearegaesargaeserete 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 MetalaleulleLeuAlaMetIleArgAlaAspSerSerGluGluLysArgHisArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 CGGCACCGGCCTCCCGGAGTCCGTCCTCGCCGCCGCCGCCGCCGCCGGGAAGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 -----GlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 CCTCCACGTCGACCCCAACCCTTCTACGGCTCCCTCTTCTCCTCCTCCTCCTCT---CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08592214A
; Sequence 17, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
    APPLICANT: Yanofsky, Martin F.
    TITLE OF INVENTION: Cauliflower Floral Meristem Identify
    TITLE OF INVENTION: Genes and Methods of Using Same
    VINTER OF SEQUENCES: 33
    CORRESPONDENCE ADDRESS: Campbell and Flores
    STREET: 4370 La Jolla Village Drive, Suite 700
    CITY: San Diego
    STATE: California
    COUNTRY: United States

ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 Arg------LysLysHisHisArgGlyTyrPhe-----
US-105-005-190-7

Patent No. 6312954

Patent No. 6312954

GRBRRAL INFORMATION.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Kinney, Tony

APPLICANT: Rafaski, Antoni

TITLE OF INVENTION.

FILE REFERENCE: BB1239 US NA DIV

GURRENT FELLING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 06/098,743

PRIOR APPLICATION NUMBER: 06/098,743

PRIOR PILING DATE: 1998-09-01.

PRIOR PILING DATE: 1998-09-01.

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Macrosoft Office 97

FERGING OF SECTION OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2335
21
7
20
34
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-10 (1-58) x US-09-668-096-9 (1-2335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.7
65.00
34.15%
25.61%
20.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
, ORGANISM: Oryza sativa
US-09-668-096-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 TTCCCT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 PhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ----
```

```
1592 GGTTTTTGCAAACAAGGGAAACCAGCTTTAGCTTTTCCCTAAAACCAC-----TCTTAC 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1532 GACATTAGTACGAGATATACCAATGAGAAGTCGACACGCAAATCCTAAAGAAACCACTGT 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 GlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 --- IleArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
ITILE OF INVENTION: DNA SEGUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMet-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTHER INFORMATION: //doc= "sequence = Arabidopsis OTHER INFORMATION: thaliana AP1 gene" US-09-149-976-17
                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-10 (1-58) x US-09-149-976-17 (1-4379)
                                                                                                                                                                                                                                                                          PRIOR APPLICATION 1915
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCE/DOCKET NUMBER: P-UD 3291
TELECOMONICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N = o
OTHER INFORMATION: nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1646 CCA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 56 Pro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-103-840A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1473 ATCAAATTGTTTATTTTCATATTTTTTAAG-TCCGCAGTTTTATTAAAAAATCATGGACCC 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1532 GACATTAGTACGAGATATACCAATGAGAGTCGACACGCAAATCCTAAAGAAACCACTGT 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 GlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ---IleArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetLysilePheilePheValPheileMetAlaLeuIleLeuAlaMet-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
COCATION: 1..4379
OTHER INFORMATION: /note= "sequence = Arabidopsis
US-08-592-214A-17
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 25-JAN-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-10 (1-58) x US-08-592-214A-17 (1-4379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
FEATURE:
NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cabiryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERSTICS:
LENGTH: 4379 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1646 CCA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 Pro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-149-976-17
```

```
US-09-328-352-3819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-359-301A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 30
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                g
                                                                                    \stackrel{>}{\circ}
                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3779614 CGTGCCCGTTCGTGCCCGTACCGCCGGCACGCCGTTGCCGCCGTCACCGCCGACGGAAC 3779555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3771728 TACCGGCGGACGCGGCCTGCCGGCG-CCGCCGCACCGCCATTGGCACCGCCGTCA 3771670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3771788 CGTGCCCGTTCGTGCCCGTACCGCCGGCGCCGTTGCCGCCGTCGCCGCCGACGGAAC 3771729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A

Sequence 1, Application US/09103840A

Patent No. 629432B

GENERAL INFORMATION:

APPLICANT: FLEISCHWAN, Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULGSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICANTION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO. 1

LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
                                                                                                                                                                                 OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LeuAsnTyr 51
                                                                                                                                                                                                                                                                                               4403765
                                                                                                                                                                                                                                                                                                                   17
15
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-10 (1-58) x US-09-103-840A-1 (1-4411529)
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-10 (1-58) x US-09-103-840A-2 (1-4403765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro
FILE REFERENCE: 24366-20007.00
CURRENT PEPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCCGGCGGCGTTCCCG 3771649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis CTHER INFORMATION: H37RV US-09-103-840A-1
                                                                                                               TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 ProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.81e+05
63.50
55.32%
36.17%
20.09%
                                                                                                                                                                                                                                                                                             8.8e+05
63.50
55.32%
36.17%
20.09%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-103-840A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                          US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
NESCHIEF APPLICATION US/09328352
Sequence 3819, Application US/09328352
Sequence 3819, Application US/09328352
Patent No. 6562958
Fatent No. 6562958
Fatent No. 6562958
FILE GALY LANTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
NUMBER OF SEQ ID NOS: 8252
LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cunagai, Monto H.
APPLICANT: della-Cioppa, Guy R.
APPLICANT: Brwin, Robert L.
APPLICANT: Brwin, Robert L.
APPLICANT: Brwin, Robert L.
APPLICANT: McGe-, David R.
TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF TITLE OF INVENTION: A DONNR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE TITLE OF INVENTION: A DONNR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE FILE REFERENCE: 008010137US04
CURRENT APPLICATION NUMBER: US/09/359,301A
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
                               3779554 TACCGGCGGACGCGGCCTGCCGCGCGGGGCCGCGCCGCATTGGCACCGCCGTCA 3779496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 ITCAGGICIGCALCAGCACICGCALAGAITITATIGGIACAGIAAAIAICAICAIAAGIA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PhellePheValPhelleMetAlaLeu-IleLeuAlaMetIleArgAlaAspSerSerGl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
-LeuAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4411
441
817
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-10 (1-58) x US-09-328-352-3819 (1-426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 rPheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
  38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro
                                                                                                                                                           3779495 cceccedececceciaricce 3779475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 uGluLysArgHisArgLysArg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-359-301A-30
; Sequence 30, Application US/09359301A
; Patent No. 6426185
; GBNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Acinetobacter baumannii
                                                                                                       52 ProProAlaTyrProPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
```

```
199 CAGGGATATCCTCAACAAGGTTATCCTCAGCAAGGATATCCTCCACCGTACGCGCCTCAA 258
                                                                                                                                                                                                                                                                                                                                                                                         35 ArgGlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mukerji, P.
APPLICANT: Prieto, P.A.
APPLICANT: Prieto, P.A.
APPLICANT: Seo, A. E.-Y.
APPLICANT: Cummings, R.D.
TITLE OF INVENTION: Method for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                 750
13
10
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALFLIANG DATE: 16-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA: No. 5576300 applicable
TELECOMMUNICATION INFORMATION:
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3074
TE
                                 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                           US-10-079-754A-10 (1-58) x US-09-359-301A-30 (1-750)
                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16.52P-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-308-883-1; Sequence 1, Application US/08308883; Patent No. 5576300; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL INE:
                                                                                                           58.33%
54.17%
19.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .kr: United States
43215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 TATCCTCCACCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 TyrProPhebro 58
                                                                                                                                                 Best Local Similarity:
Query Match:
                                                                                                           Percent Similarity:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6
CITY: Col
STATE: Oh
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
```

```
UNITS:
VANE/KEY: CDS
LOCATION: 45...593
LOCATION MITHOD: DNA sequencing and restriction analysis
LOCATION MITHOD: DNA sequencing and restriction analysis
LOCATION NOTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1: is the human
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use They
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Prieto, P. A.
APPLICANT: Prieto, P. A.
APPLICANT: Beo, A. B. -Y.
APPLICANT: Seo, A. B. -Y.
APPLICANT: Cummings, R.D.
ADPRESSED: Loonie R. Drayer
ADDRESSED: About Endoratories
ADDRESSED: Abbott Laboratories
ADRESSED: Abbott Laboratories
ATREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: ||| :::::||||
105 GAGGTTCAAAACCAGAAACAACCAGGATGCCATGAAAGACCATTCTATCAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLysilePhellePhevalPhe---IleMetAlaLeuIleLeuAlaMetIleArgAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AspSerSerGluGluLysArgHisArgLysArgLysAjsHisHisArgGlyTyrPheGln 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B)COMPUTER: Apple Macintosh OPERATING SYSTEM: MacIntosh System 7.1(D)SOFTWARE: ClarisWorks 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProProAlaTyrProPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              857
117
123
14
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-10 (1-58) x US-08-308-883-1 (1-857)
ORGANELLE:
:MMEDIATE SOURCE: Human Mammary Gland
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER: PCT/W093/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-730-163-1; Sequence 1, Application US/08730163; Sequence 1, Application US/08730163; Patent No. 5712250; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: United States 43215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7
63.00
50.85%
28.81%
19.94%
                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 625
TTTY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-308-883-1
                                                                                                                                                                                                                                                                                                                                                                                 ISSUE:
PAGES:
DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProProAlaTyrProPhe 57
                                                                                                                                                           Sequence 1, Application US/08256799;
Patent No. 622094;
Patent No. 622094;
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROEMQVIST, Mats
APPLICANT: BREGSTROEM, Sven
APPLICANT: TOernell, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: DNA ENCODING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: WASHINGTON
CITY: WASHINGTON
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FLING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FLING DATE: 23-JAM-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HANSSON=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HAN:
TELECOMMUNICATION INFORMATION:
TELEPHAN: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 857 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
45..104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594..848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13..44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-256-799-1
                                                                                                                                   RESULT 15
US-08-256-799-1
                                                             ò
                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: 'L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 ATGAAGAGTTITCTTCTAGTTGTCAATGCCCTGGCATTAACCCTGCCTTTTTGGCTGTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AspSerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGln 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetLysilePheilePheValPhe---IleMetAlaLeulleLeuAlaMetIleArgAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BATURE:
NAME/KEY:
CDS
LOCATION: 45...593
LOCATION: 45...593
LOCATION: The encoded product of nucleotide SEQ ID NO: 1:
PUBLICATION INFORMATION:
AUTHORS: L. Honsson et al
AUTHORS: L. Honson et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-10 (1-58) x US-08-730-163-1 (1-857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL LINE:
CRGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
CLONE:
CLONE:
                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear MOLECULE TYPE: cDNA DESCRIPTION: Human milk kappa-casein
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE:
CLASSIFICATION: 435
FRICK APPLICATION MURBE: US/08/308,882
FILING DATE: 16-SEP-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEX: NO. 5712506
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LINGTH: 857 Dage pairs
TYPE: NUCleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER: PCT/WO93/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
US-08-730-163-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
ANTI-SENSE:
FRAGNENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: Homo sapiens
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7
63.00
50.85%
28.81%
19.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

```
20 AspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGln 39
                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                            US-10-079-754A-10 (1-58) x US-08-256-799-1 (1-857)
       11.7
63.00
50.85%
28.81%
             Score:
Percent Similarity:
Best Local Similarity:
Query Match:
3
Alignment Scores:
Pred. No.:
                                                                            ò
                                                                                         g
                                                                                                                         d
                                                                                                                                          à
                                                                                                            Š
```

Search completed: August 16, 2004, 00:49:11 Job time : 1484 secs

Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence

Sequence

Seguence

Sequence 5, Appli Sequence 167, App Sequence 1193, Ap

Title: Perfect score:

Run on:

Sequence:

Scoring table:

```
Sequence 15, Application US/10079754A

Sequence 15, Application US/10079754A

Sequence 15, Application No. US2020164625A1

SEQUENCE 15, Application No. US2020164625A1

SEPERCANT: Glaid.

APPLICANT: Glaid.

APPLICANT: Murray R.

APPLICANT: Molenar. Adrian J.

APPLICANT: Delayer, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Occapositions ISOlated from Sovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

TITLE OF INVENTION: Murmer: US/10/079,754A

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR PILING DATE: 2000-08-22

PRIOR PILING DATE: 1000-08-22

PRIOR FILING DATE: 1000-08-23

NUMBER OF SEQ ID NOS: 15
67 14 US-10-079-754A-15

67 14 US-10-079-754A-15

18 14 US-10-079-754A-2

19 14 US-10-079-754A-2

19 14 US-10-079-754A-2

19 14 US-10-079-754A-5

10 US-10-079-754A-5

11 US-10-079-754A-5

12 US-10-079-754A-5

13 US-10-079-754A-5

14 US-10-079-754A-5

15 US-10-079-754A-5

16 US-10-079-754A-5

18 13 US-10-079-754A-5

19 US-10-079-754A-5

10 US-09-992-600A-5

11 US-10-079-754A-5

12 US-10-079-754A-5

13 US-10-079-754A-5

14 US-10-079-754A-5

15 US-10-079-754A-5

18 13 US-10-079-754A-5

19 US-09-992-600A-5

19 US-09-992-600A-5

19 US-09-992-600A-5

19 US-09-992-600A-5

10 US-09-992-600A-3

11 US-10-128-714-2032

12 US-10-128-714-2032

13 US-10-128-714-2032

14 US-10-128-714-2032

15 US-10-128-714-2032

15 US-10-128-714-6032

16 US-10-128-714-3032

17 US-10-437-963-89558

18 US-10-437-963-89558

19 US-09-920-300A-313

19 US-09-920-300A-313

10 US-09-920-300A-313

11 US-10-450-826-1

12 US-10-450-826-1

13 US-10-450-826-1

14 US-10-437-963-89726

15 US-10-437-963-89726

17 US-10-437-963-89726

17 US-10-437-963-89726

17 US-10-437-963-89726

18 US-10-128-41-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4 5307 21.4 3673778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5
                  000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
-MODEL=frame+ p2n: model - DEV=xlh
-MODEL=frame+ p2n: model - DEV=xlh
-MODEL=frame+ p2n: model - DEV=xlh
-UQ=/ cpn2 1/USPTO spool/US10079754/runat_06082004_181230_29453/app_query.fasta_1.199
-DB=Published_Applications_NA - QFMT=fastap - SUFFIX=rnpb - MINMATCH=0.1
-LCOPCL=0 - LOOPEXT=0 - UNITS=bits - STRAT=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-MAXIEN=0.00000000 - USER=LOGAL - OUTFRT=-pto - NORM=ext - HEAPSIZE=500 - MINLEN=0
-NAXIEN=0.00000000 - USER=US10079754 @CGN 1 1 480 @runat 06082004 181230_29453
-NCPUS - LICPUS 3 - NO MMAP - LARGEQUERY - NG GRORES 0 - WAIT - DSPELOCK=100
-LONGLOG - DEV TIMEOTT=120 - WARN TIMEOUT=30 - THRREADS=1 - ACGAPOP=10 - ACGAPOP=0.5
-FGAPOP=6 - FGĀPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                                                 August 16, 2004, 00:23:24 ; Search time 326 Seconds (without alignments) 872.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \
                                                                                                                                                                                                                                                                                                US-10-079-754A-10
316
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3225727 segs, 2453303834 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

Database :

Description

Query Match Length DB

Score

Result No.

Sequence 5, Appli Sequence 304, App Sequence 3032, Ap Sequence 6032, Ap Sequence 6032, Ap Sequence 6032, Ap Sequence 5032, Ap Sequence 5032, Ap Sequence 5032, Ap Sequence 8652, A Sequence 8652, A Sequence 313, App Sequence 313, App Sequence 313, App Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 67, Appl

Sequence 125, App Sequence 2, Appli Sequence 89616, A Sequence 89726, A

Sequence

```
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.68e-36
316.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                      44 AIGAAGAICTITAICTITGICTICAITAIGGCICTCAICCTAGCCAIGAITAGAGCIGAI 103
                                                                                                                                                                                                                                                                                                                                                                                                                          104 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 TCATCTGAAGGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerSerGluGluLysArghisArglysArglysElysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                     21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                1 MetLysilePheilePheValPheileMetAlaLeulleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 200, Application US/10079623

Publication No. US20020169302A1

GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glon, Marthew
APPLICANT: Glon, Martnay R.
APPLICANT: Glono, Martnay R.
FILE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: mammary gland and methods for their use:
FILE REPERBNOE: 11000, 104462
CURRENT APPLICATION NUMBER: US/10/079,623
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 370
SOFTWARE: PESESSEQ for Windows Version 4.0
SEQ ID NO 200
LENGTH: 267
                                                                                                                                              267
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-10-079-754A-15 (1-267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-10-079-623-200 (1-267)
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15 LENGTH: 267 TYPE: DNA ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.07e-37
316.00
100.00%
100.00%
                                                                                                                                                7.07e-37
316.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-623-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-623-200
                                                                                           US-10-079-754A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AIGAAGAICTITAICTITGICTICAITAIGGCICTCAICCIAGCCAIGAITAGAGCIGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 TACCAGCCATATCCACTATATCCACTAAATTATCCTGCGTATCCATTTCCT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
Sequence 1, Application US/10079754A

Sequence 1, Application US/10079754A

Sequence 1, Application No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their US TILE REPRENCE: 11000.1068

CURRENT APPLICATION WUMBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19

PRIOR PILING DATE: 2000-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 505

TVDE: NANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10079754A
| Publication No. US20020164625A1
| CENERAL INFORMATION
| APPLICANT: Glenn, Mutthew
| APPLICANT: Glenn, Mutthew
| APPLICANT: Glenn, Muttay R. |
| APPLICANT: Molenaar, Adrian J. |
| APPLICANT: Molenar, Adrian J. |
| APPLICANT: Molenar, Adrian J. |
| APPLICANT: Molenar, 2002-02-19 |
| FILE REFERENCE: 11000.1068 |
| CURRENT FILING DATE: 2002-02-19 |
| PRIOR APPLICATION NUMBER: US 09/699,146 |
| PRIOR PILING DATE: 1999-10-29 |
| PRIOR PILING DATE: 3000-08-22 |
| PRIOR FILING DATE: US 09/644,190 |
| PRIOR FILING DATE: US 09/644,190 |
| PRIOR FILING DATE: US 000-08-22 |
| PRIOR FILING DATE: US 000-08-22 |
| PRIOR PILING DATE: US 000-08-22 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-10-079-754A-1 (1-505)
```

```
149 ATGAAGATCTTTATCTTTATCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 208
                                                        SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln
                                                                                               269 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTCCT 322
                                                                                                                                                                       41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AATTATCCTCCTGCGTATCCATTTCCT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ASDIYrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                   US-10-079-754A-6
; Sequence 6, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.66e-31
277.00
82.61%
82.61%
87.66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Bovine US-10-079-754A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-3
                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \stackrel{>}{\circ}
                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetLysilePheilePheValPheileMetAlaLeuileLeuAlaMetileArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AIGAAGAICTITAICTITGICTICATIAIGGCTCICAICAICAGCAITAGAGCTGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetlysilePheilePheValPheileMetAlaLeuileLeuAlaMetileArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MESUL 5-
Sequence 2. Application US/10079754A
Publication No. US20020164625A1
Sequence 2. Application Nathew
Publication No. US20020164625A1
Sequence 2. Application Nathew
APPLICANT: Glenn, Matthew
APPLICANT: Molenar, Addian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERENCE: 11000.1068
FILE REPERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US 09/699,146
FRICA PRIOR APPLICATION NUMBER: US 09/699,146
FRICA PRIOR APPLICATION NUMBER: US 09/644,190
FRICA REPLICATION NUMBER: US 00.162,701
FRICA REPLICATION NUMBER: US 00,162,701
FRICA REPLICATION NUMBER: US 00,162,701
FRICA REPLICATION NUMBER: US 00,150,330
FRICA REPLICATION NUM
                                                                                                                                                                                                                                                                                                 00000
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-079-754A-10 (1-58) x US-10-079-754A-2 (1-585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-754A-10 (1-58) x US-10-079-754A-4 (1-604)
                 PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SECTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.88e-36
315.00
100.00%
98.28%
99.68%
                                                                                                                                                                                                                                                                                              2.15e-36
316.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-2
                                                                                                                                                           TYPE: DNA
CRGANISM: Bovine
US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                          Pred. No.:
```

ð

à

```
43 AndAAGAICTTAATCTTTGTCTTCATTATGGCTCTCTCTAGCCATGATTAGAGCTGAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 ATTCTTACTAATACAAGGATATTTCAACAATACCAGCCATATCAACGATATCCACTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 --------GlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetLysilePhellePheValPhelleMetAlaLeulleLeuAlaMetileArgAlaAsp
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Murmary Gland and Methods for Their Use
TITLE OF INVENTION: MUNBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525
0
1
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-10-079-754A-6 (1-525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION MALTHW APPLICANT: Grigor, Murray R.
```

```
Zhong, Mei
                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  ; SEQ ID NO 5
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-5
                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 ATGAAGATCTTTATCTTTATCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetLysilePheilePhevalPheileMetAlaLeuileLeuAlaMetileArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 TITATCITIGAAATAITATCTATACAATGATTAGCTTATGTGTCCATTGAATTAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 -----ArgGlyTyrPheGlnGln-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TyrGlnProTyrGlnArgTyrProLeuAsnTyr
APPLICANT: Molenaar, Adrian J.
APPLICANT: Bavis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPRENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR PILING DATE: 1999-00-29
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
LENGTH: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Ommary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: MUMBER: US/10/079,754A
CURRENT APPLICATION NUMBER: US 09/699,146
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 99/644,190
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SerSerGluGluLysArgHisArgLysArgLysLysHisHis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-10-079-754A-3 (1-869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION: APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.87e-15
170.50
55.13%
52.56%
53.96%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-079-754A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
```

```
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLBIC ACIDS ENCODING SAME, AND METHODS
FILE REPERENCE: 21402-416 A CURRENT APPLICATION NUMBER: US/10/210,172
                                                                                                                                                                                    26
                                                                                                                                                                                                          57
                                                                                                                                                                                                            1 TTTCAACAATACCAGCCATATGAACGATATCCACTAAATTATCCTCCTGCGTATCCA
                                                                                                                                                                                    38 PheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro
    96
118
00
00
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                              US-10-079-754A-10 (1-58) x US-10-079-754A-5 (1-96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 00/310,1
PRIOR PELING DATE: 2001-08-01
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-31
PRIOR PILING DATE: 2001-09-31
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR PILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                    Sequence 167, Application US/10210172
Publication No. US20040043928A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-08-07
APPLICATION NUMBER: 60/311,292
FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
                     112.00
100.00%
94.74%
35.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerlach, Valerie
Hjalt, Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leite, Mario
Vernet, Corine
Anderson, David
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boldog, Ferenc
Gorman, Linda
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                            셤
                                                     g
                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097 AIGAAGITCCTIGICTTIGCCTTCAICTIGGCTCTCAIGAITICCAIGAITIGGAGCTGAI 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 TCATCTGAAGAGAAATTTTTGCGTAGAATTGGAAGATTCGGTTATGGGTAT---GGCCCT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetlysilePheilePhevalPheileMetAlaLeulleLeuAlaMetileArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetLysilePhellePheValPheileMetAlaLeuIleLeuAlaMetileArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-13
PRIOR STLING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 167
LENGTH: 678
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-LU-LAWARE DATE:

US Sequence 1193,3 Application US/10104047

EMBLICATION NO. US20030236392A1

APPLICANT: HELIX ESERRCH INSTITUTE

TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA

FILE REPERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR PILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Petentin Ver. 2.1

SEQ ID NO 1193

LENGTH: 1584

TYPE: DNA

COGANISM: Homo sapiens

US-10-104-047-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 TATCAGCCAGTTCCAGAACAACCACTA---TACCCACAACCATAC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TyrginProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-10-104-047-1193 (1-1584)
                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-10-210-172-167 (1-678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.88e-06
110.00
61.82%
49.09%
34.81%
                                                                                                                                                                                                                                                                                                                                                              2.79e-06
110.00
61.82%
49.09%
34.81%
                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-104-047-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . . No .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
1157 TCATCTGAAGAGAAATTTTTGCGTAGAATTGGAAGATTCGGTTATGGGTAT---GGCCCT 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetlysllePhellePheValPhelleMetAlaLeulleLeuAlaMetileArgAlaAsp
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benjain, Stephane
APPLICANT: Benjain, HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.044 DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                        1214 TATCAGCCAGTTCCAGAACAACCACTA---TACCCACAACCATAC 1255
                                                                                                            41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438
118
17
17
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-09-992-600A-5 (1-438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                  Sequence 5, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.000281
94.50
56.36%
32.73%
29.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: polyA_signal LOCATION: 397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: polyA site LOCATION: 423..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 84.317
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 318.438
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-992-600A-5
                                                                                                                                                                                                                        RESULT 11
US-09-992-600A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
No
```

CURRENT APPLICATION NUMBER: US/09/992,095B

φ

```
84 ATGAAGTTTTTTGTTTTGCTTTAGTCTTGGCTCTCATGATTTCCATGATTAGCGCTGAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                         US-09-224-340-5
Sequence 5, Application US/09924340
publication No. US20030027248A1
publication No. US20030027248A1
publication No. US20030027248A1
papelCANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US2.REG
CURRENT FAPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
SPRIOR FILING DATE: 2001-06-25
SPRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USS.DIV
                                       186 ---GAAAAGCATCATTCATACCATATCACCACTACTACCACTTTTT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 TCACATGAAAGAGACATCATGGGTATAGAAGAAATTCCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-10 (1-58) x US-09-924-340-5 (1-438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/0992095B Publication No. US20030157485A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.000281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.50
56.36%
32.73%
29.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318..438
polyA_signal
397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 397.....
NAME/KEY: polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-992-095B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-924-340-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
NAME/KEY:
LOCATION:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetLysilePheilePhevalPheileMetAlaLeuileLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Benjamin, Stephane
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 60-091USOBDIV
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: PCT/IB01/01715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| ||||:::::: |||
144 TCACATGAAAAGAGACATCATGGGTATAGAAGAAAATTCCAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 ---GAAAAGCATCATTCATACCACTACCACTACCACTTTT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4438
113
117
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-079-754A-10 (1-58) x US-09-992-095B-5 (1-438)
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: UPatent
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09999570; Publication No. US20030170628A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.50
56.36%
32.73%
29.91%
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: polyA site
; LOCATION: 423..438
US-09-992-095B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: 3'UTR
LOCATION: 318..43
FEATURE:
NAME/KEY: polyA E
LOCATION: 397..4
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                  LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-999-570-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \delta
```

```
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 AIGAAGITITITIGTCTTTGCTTTAGICTTGGCTCTCATGATTTCCATGATTAGCGCTGAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetlysilePhellePheValPhelleMetAlaLeulleLeuAlaMetIleArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10000489
; Publication No. US20303092011A1
; GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT APPLICATION NUMBER: US/924,340
; PRIOR FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 ---GAAAAGCATCATTCATACCATATCACACTACTACTATTT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 TCACATGAAAAGAGACATCATGGGTATAGAAGAAAATTCCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4438
433
777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-079-754A-10 (1-58) x US-09-999-570-5 (1-438)
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: UPatent
SEQ ID NO 5
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.000281
94.50
56.36%
32.73%
29.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KRY: polyA signal
LOCATION: 397. 402
FEATURE:
NAME/KRY: polyA site
LOCATION: 423. 438
US-09-999-570-5
                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: 84..317
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 318..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-000-489-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
```

```
84 ATGAAGTTTTTTGTCTTTGCTTTAGTCTTTGGCTCTCATGATTTCCATGATTTAGCGCTGAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| || |||:::::: |||
144 TCACATGAAAAGAGACATCATGGGTATAGAAGAAAATTCCAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-10 (1-58) x US-10-000-489-5 (1-438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION UNDRER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFWARE: UPatent
SSQ ID NO 5
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 16, 2004, 01:12:54 Job time : 331 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.50
56.36%
32.73%
29.91%
                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                        FEATURE:
NOAME/KRY: 5.UTR
NOCATION: 1..83
NAME/KRY: CDS
LOCATION: 84..317
NAME/KRY: 9.UTR
LOCATION: 318..438
NAME/KRY: polyA_signal
LOCATION: 397..402
NAME/KRY: polyA_site
LOCATION: 423..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                              , LOCATION: 4:
US-10-000-489-5
```

```
Query Match 10.3%; Score 6; DB 3
Best Local Similarity 100.0%; Pred. No. 6.6
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                       RESULT 1
US-08-602-999A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 268, App
Sequence 268, App
Sequence 35, App
Sequence 376, App
Sequence 376, App
Sequence 3551, App
Sequence 4214, App
Sequence 5885, App
Sequence 5885, App
Sequence 3660, App
Sequence 3660, App
Sequence 3660, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16, Appi
25, Appi
25, Appi
8756, Ap
97, Appi
167, App
6490, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26, Appl
10559, A
4390, Ap
4, Appli
1934, Ap
29893, A
                                                                           August 6, 2004, 17:06:10 ; Search time 18 Seconds (without alignments) 166.350 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                        1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*

1. /ogn2 = 6/ptodata/2/iaa/5A_COMB.pep:*

2. /ogn2 = 6/ptodata/2/iaa/5B_COMB.pep:*

3. /ogn2 = 6/ptodata/2/iaa/6A_COMB.pep:*

3. /ogn2 = 6/ptodata/2/iaa/6B_COMB.pep:*

5. /ogn2 = 6/ptodata/2/iaa/PcTUS_COMB.pep:*

5. /ogn2 = 6/ptodata/2/iaa/PcTUS_COMB.pep:*

5. /ogn2 = 6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-291-922-26
US-09-489-039A-10559
US-09-134-001C-4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-336-643A-4
US-09-540-236-1934
US-09-252-991A-29893
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                                                 OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                             US-10-079-754A-10
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                  0
                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                   Word size :
                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                          Searched:
                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
```

ALIGNMENTS

```
Length 12;
                                                                                                                                                               DB 3;
                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          : 12 amino acids
amino acid
                                                                                                                                                     , MOLECULE TYPE: peptide US-08-602-999A-268
                                                                                                                                                  unknown
```

ö

Gaps

·.

0; Indels

```
10.3%; Score 6; DB 4; Length 103;
                                                                                                                                                                                                                                                                                               22 SEEKRH 27
                                                                                                                                                                                                                                                                                                                                   86 SEEKRH 91
                                                                                                                LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           APPLICANT: SPAKES, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 6; DB 4; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7261, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
                                                                                                                                   Sequence 268, Application US/09500124 Patent No. 6432920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TENEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 YPPAYP 56
51 YPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YPPAYP 6
                                        1 YPPAYP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-621-976-7261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-500-124-268
                                                                                                                         US-09-500-124-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
    ò
```

```
JAMESON, Brad
TEPPER, Mark
TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTRY: U.S.A.

CONDUTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/460,384

FILING DATE: 13-Dec-1999

CLASSIFICATION: «Unknown»

PRIOR APPLICATION: «Unknown»

PRIOR APPLICATION: «Unknown»

FILING DATE: 11-00199

FILING DATE: 11-00199

FILING DATE: 11-00199

FILING DATE: 12-00199

FILING DATE: 12-00199

FILING DATE: 12-00199

FILING DATE: 12-00199

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                  Length 95;
TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFREENCE: GENSTT. 0549F2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEB: BROWDY AND NEIMARK, P.L.L.C. STREET: 624 Ninth Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: YUN, Allen C
REGISCRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR=1A
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                  6; DB 4;
No. 36;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-460-384-35
                                                                                                                                                                                                                                                                                  Score 6;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT: 4
US-09-460-384-35
US-09-460-384, Application US/09460384;
Patent No. 6337316
GENERAL INFORMATION:
APPLICANT: EL TAYAR, Nabil
APPLICANT: BLECHNER, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                               Query Match 10.3%; Sc.
Best Local Similarity 100.0%; P:
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 37
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7261
```

```
RESULT 9
US-09-543-681A-4214

US-09-543-681A-4214

Sequence 4214, Application US/09543681A

Sequence 4214, Application US/09543681A

Sequence 4214, Application US/09543681A

Setent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION:

TITLE OF INVENTION:

DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

USABLE 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
                              Sequence 7386, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION
PAPELICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR SEQ ID NOS: 14342
SEQ ID NO 7386
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3551.

Sequence 3551.

Sequence 3551.

Sequence 3551.

Sequence 3551.

Sequence 3551.

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 03796-032

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3551

TENGEN 16.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 6; DB 4;
100.0%; Pred. No. 55;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 6; DB 4;
100.0%; Pred. No. 50;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.3
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 SSEEKR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 RADSSE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 RADSSE 95
RESULT 7
US-09-489-039A-7386
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-489-039A-7386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-134-000C-3551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Enter
US-09-134-000C-3551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                     GREEAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REPRENCE: 9710-003-998
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
LENGTH: 107
                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lubbers, Mark W.
Lubbers, Mark W.
Lubbers, Mark W.
Lucant: Dekker, James
APPLICANT: Christensson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: Holland, Ross
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: 11000.104301
FILLE REPERENCE: 11000.104301
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SEQ ID NO 376
LEMGTH: 134
TYPE: PPPT
CONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.3%; Score 6; DB 4; Length 134; Best Local Similarity 100.0%; Pred. No. 47; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 6; DB 4
100.0%; Pred. No. 39;
tive 0; Mismatches
     ; Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                       Sequence 1200, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Lactobacillus rhamnosus US-09-634-238-376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1200
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 6; Conservative
     Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 SSEEKR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEEKR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 YPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 YPPAYP 57
                                                                                                                        88 QQYQPY 93
                                                                             39 QQYQPY 44
                                                                                                                                                                                                   RESULT 5
US-09-198-452A-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL:

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NO SE SEQ ID NOS: 8344

LENGTH: 298

LENGTH: 298
                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3062

LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WALEWSKI, JOSE L.
APPLICANT: RECIO-PINNO, ESPERANZA
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 6; DB 4;
100.0%; Pred. No. 90;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 6; DB 4;
100.0%; Pred. No. 81;
tive 0; Mismatches
                            ; Sequence 3062, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-543-681A-5642
; Sequence 5642, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08605284B Patent No. 6060271 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Proteus mirabilis US-09-543-681A-5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 SSEEKR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SSEEKR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 FIFVFI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 FIFVFI 9
              US-09-134-001C-3062
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-3062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-605-284B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: GENY BREND:

APPLICANT: GENY BREND:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8060, Application US/09489039A

Sequence 8060, Application US/09489039A

Fatent No. 6610836

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
TITLE OF INVENTION:
FILE REFERENCE:
TOO-2004001

FILE REFERENCE:
2000-01-27

FRICE APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

FRICE REPLICATION NUMBER: US 60/117,747

FRIOR RIPLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8060
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 6; DB 4; Length 216; 100.0%; Pred. No. 69;
                                                                                                                         Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
o. 76;
                                                                                                                           10.3%; Score 6; DB 4;
100.0%; Pred. No. 65;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.3%; Score 6; DB 4 Best Local Similarity 100.0%; Pred. No. 76; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5885, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
, ORGANISM: Proteus mirabilis
US-09-543-681A-5885
                  LENGTH: 201
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                 105 MALILA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 FIMALI 188
                                                                                                                                                                                                                    10 MALILA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 FIMALI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 FIMALI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 FIMALI 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-489-039A-8060
                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-543-681A-5885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-8060
                                                                                    US-09-543-681A-4214
SEQ ID NO 4214
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                              g
```

```
299 LILAMI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LILAMI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09097889

Sequence 25, Application US/09097889

Sequence 25, Application US/09097889

Sequence 25, Application

APPLICANT Hernetadt, Corrina

APPLICANT Ghosh, Sounitra S.

APPLICANT Bavis, Robert E.

TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

COUNTRY: Seattle

STATE

ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: Patentin Release #1.0, Version #1.30
SOSTWARE: Patentin Release #1.0, Version #1.30
SOSTWARE: PEPPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: BRAWAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELEPOMINICATION INFORMATION:
TELEPHONE: 716-263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ATRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRAILING SISIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSENMAN Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.3%; Score 6; DB 3;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 FIMALI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 FIMALI 72
                                          NEW YORK
ROCHESTER
                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-605-284B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-097-889-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHRACATERISTICS:
; TYPE: amino acid
; TYPE: a
```

```
August 6, 2004, 17:09:05; Search time 46 Seconds (without alignments) 395.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                            US-10-079-754A-10
58
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291235
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGO
                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                       Run on:
```

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 7, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 70822, Sequence 586, Appli Sequence 168, Appli Sequence 168, Appli Sequence 168, Appli Sequence 168, Appli Sequence 257786, Sequence 1, Appli Sequence 268, App Sequence 170, App Sequence 164611, Description 3 US-10-079-754A-7 3 US-10-079-754A-10 3 US-10-079-754A-8 3 US-10-079-754A-9 3 US-10-079-754A-9 3 US-10-079-754A-9 3 US-10-079-754A-11 2 US-10-079-754A-11 2 US-10-079-754A-11 2 US-10-079-754A-11 2 US-10-079-754A-11 2 US-10-079-754B-11 4 US-10-424-599-145633 4 US-10-112-170 2 US-10-112-170 2 US-10-172-170 2 US-10-172-170 SUMMARIES Query Match Length DB Result No.

equence 774		equence 156	2		9 178	quence 47763,	e 225	equence 16905	equence 26634	91,	224333	e 1200,	5237,	6	a 27934	19741	21609	equence 1	equence 1	equence 73863,	205,	159623	_	equence 20348	27979		Sequence 200341,
S-09-864-4 S-10-424-5	-125-258-5 -125-258-6	8-10-424-599-15679	0-424-599-2212	-10-424-599-25083	10-437-963-17	-864-761-4	10-424-599-22582	10-424-599-1	-424-599-26	19-833-245-79	10-424-599-22	89-762-	09-738-626-623	US-10-424-599-2	US-10-424-599-27	US-10-424-5	US-10-424-599-21	US-10-424-59	US-10-437-96	US-10-282-122A-738	US-10-001-85	US-10-424-59	US-10-424-599-	US-10-424-599-20348	US-10-424-599-2797	US-10-408-765A-2	US-10-437-963-200341
11	14	177	12	12	16	σ	12	12	12	11	12	15	σ	12	12	12	12	12	16	12	13	12	12	12	12	16	16
56 62	63	7.5	71	71	72	75	81	96	99	106	0	0	108	ч	ч	114	\vdash	ч	N	$^{\circ}$	ന	マザ	ഥ	v	161	vo	161
10.3	010					10.3	•		10.3	•	10.3		10.3				•				٠			•	10.3	•	
wω	ww	o vo	v	Q	9	Q	9	9	9	9	9	9	9	9	9	9	φ	`θ	9	9	9	9	9	φ	ø	ø	6
16	80 0	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
0; Gaps
        US-LO-U-J-S-AS-A-I
S SEQUENCE 7, Application US/10079754A
Publication No. US20020164625A1
SEQUENCE 7, Application US/10079754A
Publication No. US20020164625A1
S GENERAL INFORMATION:
APPLICANT: Glenn, Marthew
APPLICANT: Glenn, Marthew
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT PPLICATION NUMBER: US/10/079,754A
CURRENT PILING DATE: 2002-02-19
PRIOR PPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR PELING DATE: 1999-08-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 58; DB 13; Length 58; Best Local Similarity 100.0%; Pred. No. 6.9e-53; Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-754A-7
US-10-079-754A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

. 0

```
8 FIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                             Sequence 12, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10079754A publication No. US20020164625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-9
         ò
                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKKHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                     Sequence 10, Application US/10079754A

Sequence 10, Application US/10079754A

Publication No. US20020164625A1

September 11 NPORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Davis, Stephen R.
ITILE OF INVENTION: Compositions Isolated from Bovine
ITILE OF INVENTION: Compositions Isolated for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/79,754A

PRIOR PELING DATE: 2000-10-27

PRIOR PELING DATE: 2000-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-00-23

PRIOR PILING DATE: 2000-08-22

PRIOR PILING DATE: 1999-08-23

PRIOR PILING DATE: 2000-08-22

PRIOR PILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Grigor, Marray R.
APPLICANT: Grigor, Marray R.
APPLICANT: Grigor, Marray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
CURRENT PELICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cn 100.0%; Score 58; DB 13; Length 58; 1 Similarity 100.0%; Pred. No. 6.9e-53; 58; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.9%; Score 51; DB 13; L
llarity 100.0%; Pred. No. 1.4e-45;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10079754A
Publication No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Mathew
APPLICANT: Grigor, Murray R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Bovine US-10-079-754A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10-079-754A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
8 FIMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Momber: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 1999-08-22
PRIOR APPLICATION NUMBER: US 00.150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TATLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: MAMMER: 1000.1068
CURRENT FILING DATE: 1000.1068
CURRENT FILING DATE: 2002-02-19
FRIOR APPLICATION NUMBER: US 60,162,701
FRIOR APPLICATION NUMBER: US 60,162,701
FRIOR PELING DATE: 1999-10-29
FRIOR PELING DATE: 1999-10-29
FRIOR PELING DATE: 1999-08-22
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 60,150,330
FRIOR PELING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.6%; Score 34; DB 13; Length 59; 100.0%; Pred. No. 7.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.6%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 7.2 Matches 34; Conservative 0; Mismatches
```

```
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pena, Carol
Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson, David
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boldog, Ferenc
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corine
                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhons,
Gerlach, Va.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leite, Mario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li, Li
Ji, Weizhen
                                                                                                                      51 YPPAYPFP 58
                                                                                                                                                            78 YPPAYPFP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 KRHRKRK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KRHRKRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vernet,
US-10-425-114-70822
                                                                                                                                                                                                                                               US-09-876-904A-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-210-172-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                           à
                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 70822, Application US/10425114

| Publication No. US20040034888A1
| Publication No. US2004003488BA1
| Publication No. US200400348BBA1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Chou, Yihua
| APPLICANT: Cao, Yongwei
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement
| TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement
| TITLE OF INVENTION: NUMBER: US/10/425,114
| CURRENT APPLICATION NUMBER: US/10/425,114
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 73128
| LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                     ó,
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grain, Macticay R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TILE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                        Query Match 46.6%; Score 27; DB 13; Length 70; Best Local Similarity 100.0%; Pred. No. 1.6e-20; Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANIEM: Zea mays
PERATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73150C02_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%; Score 11; DB 13; I 100.0%; Pred. No. 0.00027; iive 0; Mismatches 0;
                                                                                                                               8 FIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                   8 FIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                      US-10-079-754A-11
; Sequence 11, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.0
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 RYPLNYPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Bovine
US-10-079-754A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-70822
      US-10-079-754A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
Out-10 -10-10 Canal State | 13.8 % | Score 8; DB 12; Length 363; Matches | 13.8 % | Score 8; DB 12; Length 363; Matches | 13.8 % | Score 8; DB 12; Length 363; Matches | 15.0 Canservative | 10.00%; Pred. No. 4.4 % | Manatches | 10.00%; Pred. No. 4.4 % | Natural State | 10.00%; Pred. No. 4.4 % | Natural State | 10.00%; Pred. No. 4.4 % | Natural State | 10.00%; Pred. No. 4.4 % | Natural State | 10.00%; Pred. No. 4.4 % | Natural State | Natural S
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Alou Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 92-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ENO ID NO 257786
LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-927-436-1

Sequence 1, Application US/09927436

Sequence 1, Application US/09927436

Sequence 1, Application US/09927436

Sequence 1, Application US/09927436

Sequence 1, Application Sepace

APPLICANT: Amshey, Joseph W.

APPLICANT: Rooney, Regina

TITLE OF INVENTION: Highly Homogeneous Molecular Markers for Electrophoresis

FILE REFERENCE: 0942-5300001

CURRENT FILING DATE: 2001-08-13

PRIOR PRIDICATION NUMBER: US/09/927,436

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 1

LENGTH: 12

LENGTH: 12
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 7; DB 12; Length 150; 100.0%; Pred. No. 22; tive 0; Mismatches 0; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_74804C.1.pep
US-10-424-599-257786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(150)
OOTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD_RES
OTHER INFORMATION: (2)
OTHER INFORMATION: Modified with fluorescein
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (5). (5)
CTHER INFORMATION: Modified with fluorescein US-09-927-436-1
Mismatches
                                                                                                                                                                                                                                                                                 ; Sequence 257786, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.1
Best Local Similarity 100.
Matches 7; Conservative
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LAMIRAD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 LAMIRAD 26
                                                                                                                    47 irirvri 53
                                                                3 IFIFVEI 9
                                                                                                                                                                                                                                                         US-10-424-599-257786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
   Matches
                                                                ò
                                                                                                                              셤
      APPLICANT: Elleman, Azeren
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook III, John
APPLICANT: Legley, Denise et al.
APPLICANT: Logley, Denise et al.
APPLICANT: Logley, Denise et al.
APPLICANT: Logley, Denise et al.
APPLICANT: 2000-08-01
APPLICANTON NUMBER: 60/309,501
APRIOR PELING DATE: 2001-08-02
APRIOR PELING DATE: 2001-08-03
APRIOR PELING DATE: 2001-08-03
APRIOR PELING DATE: 2001-08-03
APPLICATION NUMBER: 60/310,591
APRIOR PELING DATE: 2001-08-03
APRIOR PELING DATE: 2001-08-03
APRIOR APPLICATION NUMBER: 60/310,591
APRIOR APPLICATION NUMBER: 60/310,591
APRIOR APPLICATION NUMBER: 60/310,591
APRIOR APPLICATION NUMBER: 60/312,992
APRIOR APPLICATION NUMBER: 60/312,992
APRIOR APPLICATION NUMBER: 60/312,892
APRIOR APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 145633, Application US/10424599
Sequence 145633, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENDENCE: 38-21(53.23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145633
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 12; Length 72; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102525C.1.pep
US-10-424-599-145633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 ADSSEEK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSSEEK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-424-599-145633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
20 DSSEEK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-210-172-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                          Gaps
                                            ;
0
                                                                                                                                                                                                                                                                                                           APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUTLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York.
CHARLES OF SECURICAL AND CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                          0; Indels
  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
PILING DATE: CLASSIFICATION DATA:
PILING DATE: US/10/161,791
FILING DATE: US/10/161,791
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-196
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (212) 790-9090
Query Match 10.3%; Score 6; DB 5
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                 Sequence 268, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; SCUL.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOC ""
SOFTWARE: Party
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-10-161-791-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 YPPAYP 56
                                                                                    29 KRKKHH 34
                                                                                                                             3 KRKKHH 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-210-172-170
; Sequence 170, App
; Publication No. U
```

```
APPLICANT: Malyankar, Dates
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TILLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-416 A 19/210,172
CURRENT APPLICATION NUMBER: 60/329,501
PRIOR APPLICATION NUMBER: 60/329,501
PRIOR APPLICATION NUMBER: 60/319,814
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,911
PRIOR PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,911
PRIOR APPLICATION NUMBER: 60/310,911
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR APPLICATION NUMBER: 60/311,999
PRIOR APPLICATION NUMBER: 60/311,999
PRIOR APPLICATION NUMBER: 60/311,999
PRIOR APPLICATION NUMBER: 60/311,999
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,999
PRIOR PILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 327 SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 6; DB 1:
100.0%; Pred. No. 89;
ive 0; Mismatches
                                                                       Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Taman, Stacie
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerlach, Valerie
Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.u
Lange 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, David
                                                                                                                                                                                                                                                                                     Boldog, Ferenc
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mei
```

```
NESULT 15
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
19-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
10-10-44-599-164611
```

```
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-962-569A-8
                                                                                                                                                                                                                                                             US-07-962-569A-8
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 21, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 27348, Ap
Sequence 27348, Ap
Sequence 27348, Ap
Sequence 27419, A
Sequence 27419, A
Sequence 20994, A
Sequence 20994, A
Sequence 30311, A
Sequence 4, Appli
Sequence 4, Appli
Sequence 279914
Sequence 279914
Sequence 164, Appli
Sequence 164, Appli
Sequence 164, Appli
Sequence 1246, Appli
Sequence 1246, Appli
Sequence 1246, Appli
Sequence 225, Appli
Sequence 225, Appli
Sequence 225, Appli
Sequence 1246, Appli
Sequence 1246, Appli
Sequence 1246, Appli
Sequence 1246, Appli
Sequence 225, Appli
Sequence 1248, Appli
                                                                         6, 2004, 17:04:44; Search time 18 Seconds (without alignments) 166.350 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8
                                                                                                                                          1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
    /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-284-465-6
US-09-489-039A-9137
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                               389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
             GenCore.version (c) 1993 - 2004
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum.Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                US-10-079-754A-10
316
                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                     Copyright
                                                                             August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
63
63
63
61.5
61.5
                                                                                                                                                                Scoring table:
                                                        OM protein
                                                                                                                                             Sequence:
                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
```

```
29 55.5 17.6 69.9 4 180-90-222-918-240.2 Sequence 20.4042, Applia 55.5 17.6 64.4 10.09-222-918-240.2 Sequence 20.4042, Applia 55.5 17.6 64.4 10.09-222-918-240.2 Sequence 20.4042, Applia 55.5 17.6 64.4 10.09-222-918-240.2 Sequence 20.404.2 Sequenc
```

```
RESULT 3
US-08-730-163-2
Sequence 2, Application US/08730163
Sequence 2, Application US/08730163
Sequence 1. Application US/08730163
Sequence 2. Application US/08730163
Sequence 2. Application US/08730163
Sequence 3. Application US/08730163
Sequence 3. Application US/08730163
Sequence 3. Application US/08730163
Sequence 3. Application US/08730163
STILLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.
NUMBER OF EXQUENCES: 2
SUCRESSED: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbort Laboratories
STREET: 625 Clawland Avenue
CITY: Columbus
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ohio
COUNTRY: United States
COUPTRY: United States
COUPTRY: United States
COUPTRY: United States
COUPTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B) COMPUTER: Apple Macintosh
OPERATION SYGTEM: Macintosh System 7.1(D) SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE:
CLASSIFFCATION: 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,882
FILING DATE: 16-SEP-1994
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKSFILVVNALALTIDFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DCCUMENT NUMBER: PCT/W093/15196
; FILING DATE: 25-JAN-1993
; PUBLICATION DATE: 05-AUG-1993
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-308-883-2
                                                                                                                                                                              R: PCT/WO93/15196
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein.
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL:
                                             RESULT 2
US-08-308-883-2
US-08-308-883-2
Sequence 2, Application US/08308883
Sequence 2, Application US/08308883
GENERAL IMPORMATION:
APPLICANT: Wakerli, P.
APPLICANT: Prieto, P. A.
APPLICANT: Cummings R.-Y.
APPLICANT: Cumming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States
ZIP: 4315
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYTEM: Macintosh
OPERATING SYTEM: Macintosh
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
PRICR APPLICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE TRACTERISTICS:
LINEAR AMINO acid
TYPE: Linear
MOLECULE TYPE: Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE:
TISSUB TYPE:
CELL LIVE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBBARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Col
STATE: OF
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
```

```
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKIFIEVF-IMALILAMIRADSSEEKRHRKKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                    1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HANSON, Lennart
APPLICANT: STROEMOVIST, Mats
APPLICANT: STROEMOVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HENNELL, Olle
APPLICANT: HENNELL, Olle
APPLICANT: PORNELL, Olle
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                         ; Score 63; DB 3; Length 182;
; Pred. No. 2.3;
13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 63; DB 3; Length 182; 28.8%; Pred. No. 2.3; ative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: ZUCY BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: OS-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DS 88/92
FILING DATE: 23-JAN-1992
ATTONEY/AGENT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HANSSON=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-462-437-2; Sequence 2, Application US/08462437; Patent No. 6232094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPERBNCE/DOCKET NUMBER: HP
TELECOMONINICATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.8%;
Matches 17; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 182 amino acids
TYPE: amino acid
                                           TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.8 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-799-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-462-437-2
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                   Process for Obtaining the Protein and Use The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKHHRGYFQCYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKSFLLVVNALALTLPFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 2. Application US/08256799
| Patent No. 6222094
| Patent No. 6222094
| GENERAL INFORMATION:
| APPLICANT: HANSSON, Lennart
| APPLICANT: STROEMOVIST, Mats
| APPLICANT: HEXBELL, Olle
| APPLICANT: HEXBELL, Olle
| APPLICANT: Toernell, Jan
| TILE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
| UNMER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESSES: REOWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.9%; Score 63; DB 1; Length 182; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 17; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: TEACHED FOR MEAN MEDIUM TYPE: FILOPOW disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/256,799 FILING DATE: 06-DEC-1994 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: DK 88/92 AFLING DATE: 23-JAN-1992 ATTORNEY/AGENT INFORMATION: NAME: COOPER, IVET P. REGISTRATION NUMBER: P. REFERENCE/DOCKET NUMBER: HANSSON=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                    NATURATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, P?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R: PCT/WO93/15196
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER: PCT/WO93/15190
FILING DATE: 25-JAN-1993
BUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
     CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                              UNITS:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-256-799-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-730-163-2
```

à

```
Score 62;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-625-188-20
; Sequence 20, Application US/09625188
"--ent No. 6307037
                                                                                                                 ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27856
                                                                                                                                                                                                                                                                                                             40 RHRRRRRHHRGNPQRRRP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis
                                                                                                                                                                                                                                                                             26 RHRKRKKHHRGYFQQYQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 39.5%;
Matches 17; Conservative
                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
, ORGANISM: Ashbya gossypii
US-09-625-188-20
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 27856
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-134-000C-4463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-000C-4463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 20
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27856, Application US/09252991A
Sequence 27856, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRENDE: 107196.13 6
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKSFLLVVNALALTLPFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
    1 MKSFLLVVNALALTLPFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart
APPLICANT: HANSSON, Lennart
APPLICANT: HERGSTROEM, Sven
APPLICANT: HERNELL, Olle
APPLICANT: HERNELL, Olle
APPLICANT: HERNELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, OLLE
APPLICANT: TOERNELL, OLLE
APPRICANT: DNA ENCODING KAPPA-CASEIN, PROCESS
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
UNDBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; · Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-UW-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.9%; Score 63; DB : 28.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: HANSSON=1A
TELECOMONIACATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-5528
                                                                                                                 Sequence 31, Application US/08462437 Patent No. 6232094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.8%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: COOPER, IVER P. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 182 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-462-437-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                     -08-462-437-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
            g
```

```
Sequence 4463, Application US/09134000C

Sequence 4463, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICATION DOUGETE-Stamm et al

TILLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TILLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NOS: 6812

SEQ ID NO 4463

LENGTH: 620
                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
;-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 729;
Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LILAMIRADSSEEKRHRKR----KKHHRGYFQQYQPY-QRYP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LLLKSIK----KSLRHRRRIPMQTKKIHFGAFSRFKPYLLRYP 54
                                                                                                                                                                                                                                                                                                  GENERAL INCORMATION:
APPLICANT:
APPLICANT:
No. 6307037artis AG
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REPERENCE: PB/5-31285P1
CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 SQQSQAHSQQHQQQQQQQQQQQQQQQQQQQQQPPQQP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SSEEKRH-RKRKKHHRGYFQQYQPYQRYPLNYPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61; DB 4;
Pred. No. 15;
  4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.5%; Score 61.5; D
Best Local Similarity 32.4%; Pred. No. 16;
Matches 12; Conservative 9; Mismatches
DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                             5; Mismatches
```

```
18 RADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLN
CURRENT FILING DATE: 1999-02-18
PRIOR PEDICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21881
LENGTH: 720
                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                  18.7%; & milarity 29.8%; E Conservative 8;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-252-991A-20994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-27419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Pseudo
US-09-252-991A-20994
                                                                                                                                                                                                                                                                        US-09-252-991A-21881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                 Sequence 16848 Application US/09252991A

Sequence 16848 Application US/09252991A

Patent No. 655195

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

ABRIGATION ABRIGATION ABRIGATION ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

ABRICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16848

LIENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27348
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-21881

Sequence 21881, Application US/09252991A

Sequence 21881, Application US/09252991A

Sequence 21881, Application US/09252991A

SEQUENCE SESTIPS

PATENT INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :|||:||:||:||
| RAD---RQRHRRRRRYHFRRADRGQRGPAQDSPRGQPRQEQPGQAGEDPPA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RGYFQQYQPYQ-RYPLNYPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59.5; DB 4; Length 271;
Pred. No. 9.4;
8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59, DB 4; Length 225;
Pred. No. 8.9;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQAGEQVRORRKEDAADQGEARQTVEPPOFHPLAIDPAYP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 ADSSEEKRHRKRKKH--HRGYFQQ-YQPYQRYPLNYPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-252-991A-27348
; Sequence 27348, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%;
39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 RADSSEEKRHRKRKKHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.08
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-27348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
Sequence 2094, Application US/09252991A

Sequence 2094, Application US/09252991A

Patent No. 655175

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC AID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/00/18
PRIOR APPLICATION NUMBER: US/00/190
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20994

LENGTH: 333
                                                                                                                                                                                                                                                              Sequence 27419, Application US/09252991A
Sequence 27419, Application US/09252991A
Sequence 27419, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
ო
                                                           10;
                                                                                                                                                       325 RAGQQPQRRHRQQRRHHPGGRPAGQRPAGTGQRQGPARRQPERPRPA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 247;
     Length 720;
                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                18 RADSSEEKRHRKRKKHH------RGYFQQYQPYQRYPLNYPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.5%; Score 58.5; DB 4;
Best Local Similarity 39.4%; Pred. No. 11;
Matches 13; Conservative 6; Mismatches 11;
Score 59; DB 4;
Pred. No. 32;
8; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
```

```
RESULT 15

US-09-252-91A-30311

Sequence 30311, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30311

LENGTH'S 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                              1,
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Query Match
18.5%; Score 58.5; DB 4; Length 333;
Best Local Similarity 38.7%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
18.4%; Score 58; DB 4; Length 521;
Best Local Similarity 36.7%; Pred. No. 30;
Matches 18; Conservative 6; Mismatches 21; Indels
                                                                                                                                                25 KRHRKRK---KHHRGYFQQYQPYQRYPLNYP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-30311
```

Search completed: August 6, 2004, 17:05:15 Job time: 19 secs

g

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

August 6, 2004, 17:04:44 ; Search time 47 Seconds (without alignments) 387.098 Million cell updates/sec

US-10-079-754A-10 316 1 MKIFIFVFIMALILAMIRAD......QQYQPXQRYPLNYPPAXPFP

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1291235 seqs, 313682936 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/DCT_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/DCT_MW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/DCT_MW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 12, Appl	Sequence 9, Appli	Seguence 11, Appl	Sequence 168, App	Sequence 19, Appl	Sequence 6, Appli						
QI	US-10-079-754A-7	US-10-079-754A-10	US-10-079-754A-8	US-10-079-754A-12	US-10-079-754A-9	US-10-079-754A-11	US-10-210-172-168	US-09-917-340-19	US-09-992-600A-6	US-09-924-340-6	US-09-992-095B-6	US-08-999-570-6	US-10-000-489-6	US-10-000-986-6	US-10-154-678-6
	13	13	13	13	13	13	12	σ	10	10	10	10	14	14	14
% Query Match Length DB	58	28	28	59	70	21	62	51	78	78	78	78	78	78	78
Query Match	100.0	100.0	99.7	53.8	53.5	35.4	34.8	30.1	29.9	29.9	29.9	29.9	29.9	29.9	29.9
Score	316	316	315	170	169	112	110	95	94.5	94.5	94.5	94.5	94.5	94.5	94.5
Result No.	-	8	m	4	S	9	7	00	σ	10	11	12	13	14	15

ö

1 MXIFIEVPIMALILAMIRADSSEEKRHRKKKKHHRGYFQQYQPYQRYPLNYPPAYPPP 58 1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAYPFP

d

Sequence 192104,	equence 1	e 193	quence	equence 193	22,	197	192	193	188	4	19213	13	19209	14	1459,	equence 19215	equence 19221	17953	equence 19	19199	19205	9216	equence 19209	equence 19210	17	e 19217	e 15	ce 1	Sequence 192165,
US-10-437-963-19210	US-10-437-963-19217	US-10-437-963-19204	US-10-282-122A-71	US-10-437-963-19209	US-10-631-581-2	US-10-437-963-19198	US-10-437-963-19210	US-10-437-963-191	US-10-437-963-18810	US-10-374-78	US-10-437-963-192	US-10-437-963-19207	US-10-437-963-192	US-10-374-780A-14	US-10-374-780A-14	US-10-437-963-19215	US-10-437-963-192	US-10-437-963-17953	US-10-437-963-19205	US-10-437-963-19199	US-10-437-963-192	US-10-437-963-192	US-10-437-963-19209	US-10-437-963-19210	US-10-437-963-17954	US-10-437-963-19217	US-10-437-963-19210	US-10-437-963-1	US-10-437-963-19216
16	16	16	12	16	16	16	16	16	М	Н	Н	Н	Н	Н	٦	Н	1	٦	٦	-	Н	н	٦	Н	Н	Н	_	-	-
50	1680	36	229	1822	277	0.8	19	40	48	1504	50	51	54	56	56	57	57	59	62	68	69	73	1761	1764	1776	1792	1809	1815	1820
ď.	N.	۷.	21.8	i.	o.	0	0	0	0	Ö	ö	ö	Ö	ö								ö	0	ö	o.	°.	٥.	。	
72	72	20	69	69	99	9	. 62	92	65	9	65	65	65	65	65	65	65	65	65	65	65	65	65	65	65	e S	65	65	65
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
.
0
         Query Match
Best Local Similarity 100.0%; Score 316; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                     TYPE: PRT
CRGANISM: Bovine
US-10-079-754A-7
RESULT 1
US-10-079-754A-7
```

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.8%; Score 170; DB 13; Best Local Similarity 100.0%; Pred. No. 1.1e-12; Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                            Sequence 12, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
à
                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MXIFIFVFIMALILAMIRADSSEERRHRKRKKCHHRGYFQQYQPYQRYPLAYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                        Sequence 10, Application US/10079754A

Publication No. US20020164625A1

FEBRERAL INPORMATION:
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 2000-06-22

PRIOR SPELICATION NUMBER: US 09/644,190

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORPATION:
GENERAL INCORPATION:
APPLICANT: Glenn, Marthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthen
APPLICANT: Grigor, Murray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT FILING DATE: 2000.1059
FRIOR APPLICATION NUMBER: US 69/699,146
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-00-29
PRIOR FILING DATE: 1999-00-29
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.7%; Score 315; DB 13; Length 58; Best Local Similarity 98.3%; Pred. No. 7.4e-30; Matches 57; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bovine
US-10-079-754A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-079-754A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
```

В ઠ

```
1 MKIFIFIFIMALILAMIRADSSEEKRHRKKKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Grien, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Mammary Grien Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERBYCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2000-20-19
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 12000-10-27
PRIOR PILING DATE: 2000-08-22
PRIOR PAPLICATION NUMBER: US 60,162,701
PRIOR PAPLICATION NUMBER: US 60,150,330
PRIOR PAPLICATION NUMBER: US 60,150,330
PRIOR PILING DATE: 1200-08-22
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 9
LENGTH: 70
                                                                                                                                                                                                                                                                                                    CHARALL INTEGRATION:

APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US 09/699,146
PRIOR APPLICANTON NUMBER: US 60,162,701
PRIOR APPLICANTON NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 59;
```

```
Gerlach, Valerie
Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
                                                                                                  Bđinger, Shlomit
Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-210-172-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-917-340-19
                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                      WESLO-079-754A-11

Sequence 11, Application US/10079754A

Publication No. US20020164625A1

Sequence 11, Application US/10079754A

Publication No. US20020164625A1

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Bovine

FILE REFERENCE: 11000.1068

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR PLING DATE: 1999-10-29

PRIOR PLING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR PLING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15 SOFTWARE: EastSEQ for Windows Version 4.0

SEMPLING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.4%; Score 112; DB 13; Length 21; 94.7%; Pred. No. 2.5e-06;
                                     53.5%; Score 169; DB 13; Length 70; 97.1%; Pred. No. 1.7e-12; Live 1; Mismatches 0; Indels
                                                                                                                              1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                 1 MKIFIFIFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURTON 10210172

Sequence 168 Application US/10210172

Publication No. US20040043928A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Miller, Charles

APPLICANT: Patturajan, Meera

APPLICANT: Presen, Carol

APPLICANT: Rieger, Daniel

APPLICANT: Shinkets, Richard

APPLICANT: Zerbusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 FOOYOPYORYPLNYPPAYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOOYOPYERYPLNYPPAYP 19
                                Ouery Match
Best Local Similarity 97.1;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boldog, Ferenc
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, Da
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-754A-11
US-10-079-754A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
```

```
PAPLICANT: Bleaman, Kareen
APPLICANT: Malyankar, Uriel
APPLICANT: Stock of II, John
APPLICANT: Alsobook II, John
APPLICANT: Alsobook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

34.8%; Score 110; DB 12; Length 62;
Best Local Similarity 49.1%; Pred. No. 1.4e-05;
Matches 27; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09917340
; Sequence 19, Application US/09917340
; Patent No. US2002009369A1
; GENERAL INFORMATION:
APPLICANT: MULPDY, Christopher J.
APPLICANT: MCADULLY, Jonathan F.
APPLICANT: McADULLY, Jonathan F.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT FILING DATE: 2001-07-29
FRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR PILING DATE: 2000-11.7
; PRIOR FILING DATE: 2000-105-15
; RIOR FILING DATE: 2001-05-15
```

```
; Sequence 6, Application US/09999570; Publication No. US20030170628A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-924-340-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-992-095B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-992-095B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-999-570-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNYPPAY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
ITILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.034.DIV
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PILING DATE: 2001-01-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-06-29
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.9%; Score 94.5; DB 10; Length 78; 32.7%; Pred. No. 0.0012; tive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09924340
Publication No. US20030027248A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
ITILE OF INVENTION: HUWAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US2.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
                                                                                                                                                                                                                                                                                                                                                                                                        1 MKFFVFALILALMLSMTGADSHAKRHHGYKRKFHEKHHSHRGYRSNY 47
                                                                                                                                                                                                                            Query Match 30.1%; Score 95; DB 9; Length 51; Best Local Similarity 46.8%; Pred. No. 0.00067; Matches 22; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                               1 MKIFIFVFIMALILAMIRADSSEEKRH-RKRKKH-----HRGYFQQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION:
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 51
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.7%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: 1..19

US-09-992-600A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-992-600A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-924-340-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

```
PRIOR FILING DATE. 200.-66-29

PRIOR PLING MANDER: 036-06-15

PRIOR PLING DATE. 200.-66-15

PRIO
```

Ŋ

ä

```
1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNYPPAY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAY 55
                                                                                                                                                                                                                         --EKHHSYHITLLPLF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10154678

Publication No. US203016218641

GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hiroaki

FILE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 182.US1.REG

CURRENT FILING DATE: 200.10-15

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCRMANIA.

GENERAL INCRMANIA.

APPLICANT: Benjania,

APPLICANT: Tanaka, Hiroaki

APPLICANT: Tanaka, Hiroaki

FILTE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US9.DIV

CURRENT APPLICATION NUMBER: US/10/000,986

CURRENT APPLICATION NUMBER: US 09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
29.9%; Score 94.5; DB 14; Length 78;
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels
                                     17; Indels
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 1
                                                                                                                                                                                        1 MKFFVFALVLALMISMISADSHEKRHGYRRKFH
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/1000986 Publication No. US20030096247A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: SIGNAL

LOCATION: 1..19

US-10-000-986-6
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-000-986-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                         8
                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFFVFALVLALMISMISADSHEXRHHGYRRKFH------EKHHSYHITLLPLF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAY 55
                       APPLICANT: Designation, occupants, APPLICANT: Tanaka, Histoaki, TILLE OF INVENTION: HUMAN CDNAS AND PRCTEINS AND USES THEREOF TILLE REFERENCE: G-091US08DIV CURRENT APPLICATION NUMBER: US (09/999,570 CURRENT APPLICATION NUMBER: US (09/924,340 PRIOR PRICATION NUMBER: US (09/924,340 PRIOR PLICATION NUMBER: PCT/IBO1/01715 PRIOR PLING DATE: 2001-08-06 PRIOR PRILING DATE: 2001-08-06 PRIOR APPLICATION NUMBER: PCT/IBO1/01715 PRIOR APPLICATION NUMBER: US 60/305,456 PRIOR PRILING DATE: 2001-07-13 PRIOR PILING DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-25 PRIOR PRILING DATE: 2001-06-15 PRIOR PILING DATE: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.9%; Score 94.5; DB 10; Length 78; Best Local Similarity 32.7%; Pred. No. 0.0012; Matches 18; Conservative 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10000489
Publication VO. US20030092011A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION WUMBER: US 09/924,340
PRIOR APPLICATION WUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION WUMBER: US 60/302,277
PRIOR RILING DATE: 2001-06-29
PRIOR APPLICATION WUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
NUMBER OF SQQ ID NOS: 112
SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/000,489 CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.98;
    APPLICANT: Benjanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-10-000-489-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-999-570-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

1;

Sequence 17, Appli Sequence 20, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli

Sequence 1, Sequence 1,

Sequence 30, Sequence 28, Sequence 17, Sequence 17, Sequence 17,

Sequence 71, Sequence 71, Sequence 33,

Sequence 33, Sequence 34, Sequence 38,

Seguence Sequence

Sequence 38, Sequence

us-10-079-754a-10.rni

```
Sequence 56, Application US/08434099A

Patent No. 6083902

GENERAL INFORMATION:

APPLICANT: Cederholm-Wms., Stewart A.

TITLE OF INVENTION: Recombinant Fibrin Chains,

TITLE OF INVENTION: Fibrin and Fibrin-Homologs

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: E.R. Squibb & Sons, Inc.

STREET: 100 Headquarters Park Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-486-663A-17

US-08-47-904B-7

US-08-435-637A-1

US-08-435-637A-1

US-08-435-637A-1

US-08-434-38-1

US-08-632-580A-3

US-08-632-580A-3

US-08-632-580A-3

US-08-955-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-96-171E-37

US-08-96-171E-37

US-08-96-171E-37

US-08-96-171E-38

US-08-96-171E-38

US-08-195-073-28

US-08-195-073-28

US-08-195-073-28

US-08-195-073-28

US-08-195-073-28

US-08-195-073-28

US-08-195-073-28

US-08-441-107-38

US-08-441-107-31

US-08-481-710-33

US-08-481-710-33
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Furman, Jr., Esq., Theodore R
REGISTRATION NUMBER: 30,942
REFERENCE/DOCKET NUMBER: CV0054a
TELECOMMUNICATION IRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 908-281-2373
TELEX:
                                                                                                                          1830121
                                                                                                                                     1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skillman
   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-434-099A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: STATE:
                                                                                                                                                   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
      0000 0000
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Appli
Sequence 5, Appli
Sequence 1950, Ap
Sequence 1868, Ap
Sequence 2340, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 28, Appli
                                                                                     August 16, 2004, 00:50:06; Search time 61 Seconds (without alignments) 527.658 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                  US-10-079-754A-10
58
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-434-099A-26
US-08-206-176-5
US-09-543-681A-1164
US-09-134-000C-1868
US-09-543-681A-2340
US-09-543-681A-2670
US-09-543-681A-2670
US-08-56-647B-3
US-08-237-401A-3
US-08-100-692-4
US-08-106-30-4
US-08-674-030-4
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                60.0
60.0
7.0
                                                                                                                                                                                               60.0 , Ygapext 6
60.0 , Ygapext 6
6.0 , Fgapext
6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1438
10564
11062
11509
12082
2437
25598
25598
2619
                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
                                                                                                                                                                                             Xgapop (Ygapop (Fgapop
                                                                                                                                                                                    OLIGO
                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                ı
                                                                OM protein
                                                                                                                                                                                                                                                                                    Word size:
                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                       Run on:
```

us-10-079-754a-10.rni

```
.5-08-206-176-5
; Sequence 5, Application US/08206176
; Patent No. 563940
; GENERAL INFORMATION:
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donna E
APPLICANT: Foster, Donna E
APPLICANT: Foster, Donna C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
SIRRE: Seattle
CITY: Seattle
CITY: Seattle
SIRTE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-10 (1-58) x US-08-434-099A-26 (1-1438)
                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Parker, Gary B
REGISTRATION NUMBER: 31-648
REPERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-549-2808 ext 322
TELEPHONE: 206-549-2808
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 MetAlaLeuIleLeuAlaMetIle 17
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 1438 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear FEATURE:
                                                                                                                                                 NAME/KEY: Coding Sequence
LOCATION: 3...1364
OTHER INFORMATION:
US-08-434-099A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
13.79%
                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                core:
```

```
Sequence 2950, Application US/09543681A

APPLICANT: GARY BRETON

TITLE OF INVENTION: UDIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

TITLE OF INVENTION: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2950

LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: ULOSOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENY APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 2000-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NO: 8344

LENGTH: 1062
..2603, 4211..4341, 4645..4778, 5758..5942, 7426
..7703, 9342..9571)
                                                                                       10564
8
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-10 (1-58) x US-09-543-681A-2950 (1-711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-08-206-176-5 (1-10564)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                       US-09-543-681A-1164
; Sequence 1164, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                  10 MetalaLeulleLeuAlaMetile 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 TTCATAATGGCATTGATATTG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 PhelleMetAlaLeulleLeu 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8
7.00
100.00%
100.00%
                                                                                                                          100.00%
100.00%
13.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                         RESULT 3
US-09-543-681A-2950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-543-681A-2950
   , LOCATION:
, LOCATION:
US-08-206-176-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                      à
```

Alignment Scores:

```
US-09-543-681A-2670/C

Sequence 2670, Application US/09543681A

Sequence 2670, Application US/09543681A

Sequence 2670, Application US/09543681A

Sequence 2670, Application US/09543681A

Patent No. 6605709.

GENERAL INFORMATION:

APPLICANT GARY BRETON

TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION WUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-456-647B-3/C

Sequence 3, Application US/08456647B

Sequence 3, Application US/08456647B

Patent No. 581816

GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg E.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCES: 54

CORRESPONDENCE Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-10 (1-58) x US-09-543-681A-2670 (1-2082)
                                                                       US-10-079-754A-10 (1-58) x US-09-543-681A-2340 (1-1914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-UN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFFLICATION NUMBER: US 07/884,486 FILING DATE: 15-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1399 TACCCGCCAGCGTATCCATT 1379
                                                                                                                                            669 ATCTTCATCTTCGTCTTCATC 649
                                                                                                                      3 IlePheIlePheValPheIle 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TyrProProAlaTyrProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Proteus mirabilis US-09-543-681A-2670
    12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2670
LENGTH: 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-543-681A-2340/c
US-09-543-681A-2340/c
Sequence 2340, Application US/09543681A
Factor No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNCARRIC 2009
TITLE REFERENCE: 2769.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2340
                                                                                                                                                                                                                                                                                                             US-09-134-000C-1868/C

Sequence 1868, Application US/09134000C

Sequence 1868, Application US/09134000C

Patent No. 661156

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTREACCE TO SEQUENCES PRECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

LENGTH: 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-754A-10 (1-58) x US-09-134-000C-1868 (1-1509)
                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-09-543-681A-1164 (1-1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1212 Arririariririciriricarc 1192
                                                                                                                                                                                                                                                              467 rrrarrargecacraarccra 487
                                                                                                                                                                                                                    8 PhelleMetAlaLeulleLeu 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
7.00
100.00%
100.00%
                                              100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Proteus mirabilis
                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-543-681A-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-000C-1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
    Pred. No.:
```

STRANDEDNESS: single

```
Sequence 3, Application US/08237401A; Sequence 3, Application US/08237401A; Patent No. 5837448
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEIN-IYROSINE KINASE GENES NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
PRIOR APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Halle Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 07251/00701
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-08-456-647B-3 (1-2437)
ATTORNEY/AGENT INFORMATION:

NAME: Wetherell Ph.D., John R.

REGISTRATION NUMBER: 31678

REFERENCE/DOCKET NUMBER: 07251/007002

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5070

INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2437 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ses aracricccardarcadaddc ses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 IleLeuAlaMetIleArgAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                           TOPOLOGY: linea
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
CLONE: TYPO-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
3est Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .08-237-401A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92037
                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY:
; LOCATION:
US-08-456-647B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
```

```
Sequence 4, Application US/08100692
| Sequence 4, Application US/08100692
| Patent No. 533248
| GENERAL INFORMATION:
| APPLICANT: Hubbergise, Jon M. APPLICANT: Hubbergise, Jon M. APPLICANT: Showley, Peter M. TITLE OF INVENTION: DE ASSOCIATED PROTEIN AND METHODS OF USE NUMBER OF SEQUENCES: GCORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
| STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER LA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: DREADIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,692

FILING DATE: 19930730

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: PRATHES, 31,990

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 15,280-91

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEPHONE: (206) 467-9600

TELEPHONE: (206) 467-9600

TELEPHONE: 2598 DASSE PAISE:

SEQUENCE CHARACTERISTICS:

LENGTH: 2598 DASSE PAISE
                                                                                                                                                                                                                                                                Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0
                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-10 (1-58) x US-08-237-401A-3 (1-2437)
                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 ATACTTGCCATGATCAGAGCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                 13 IleLeuAlaMetIleArgAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: sing
STRANDEL.
TOPOLOGY: linc.
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: TYPO-2
; FEATURE: TYPO-2
; NAME/KEY: CDS
; LOCATION: 3...
US-08-237-401A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-100-692-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
; LOCATION:
US-08-100-692-4
                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
APPLICANT: Hulbregtse, Jon M.
APPLICANT: Scheffner, Martin
APPLICANT: Scheffner, Martin
APPLICANT: Scheffner, Martin
APPLICANT: Howley, Peter M.
TITLE OF INVENTION: B6 ASSOCIATED PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
CORRESPONDENCE: 6
CORRESPONDENCE: 6
CORRESPONDENCE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY U.S.A.

ZIP: 94105-1492
ZIP: 94105-1492
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,030
FILING DATE: 0.-UL-1996
CLASSIPICATION NUMBER: US/08/674,030
FILING APPLICATION NUMBER: 1990
RECISTRATION NUMBER: 30-UL-1993
ATTONEY/AGENT INFORMATION:
NAME: PATENCE/DOCKET NUMBER: 1,990
REGISTRATION NUMBER: 31,990
RECOMMUNICATION INFORMATION:
TELEPRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
ILBRIGHTH: 2598 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-08-674-030-4 (1-2598)
                                                                                                             US-10-079-754A-10 (1-58) x US-08-100-692-4 (1-2598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                              543 Arcricarcrirercricard 523
                                                                                                                                                                                                                                                                            Sequence 4, Application US/08674030 Patent No. 5914389 GENERAL INFORMATION:
    100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
7.00
100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 1010..1321
US-08-674-030-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                             JS-08-674-030-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score:
```

543 ATCTTCATCTTTGTCTTCATC 523

```
REGULT 13

Organization 19(09166350A

Sequence 26, Application US/09166350A

Patent No. 6440663

Patent No. 6440664

APPLICANT: Charle No. 1000

APPLICANT: Alex Talsabeth

APPLICANT: A
```

```
US-10-079-754A-10 (1-58) x US-08-767-942A-20 (1-2624)
, LOCATION: 1..2624
US-08-247-904B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                              Alignment Scores:
                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequency 7, Application US/08247904B
Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Eckstein, Jens W.
APPLICANT: Desetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-08-486-663A-17 (1-2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: MA
COUNTRY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDLIUM TYBE: PLOBDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994
CLASSIFICATION NUMBER: MS/08/247,904B
FILING DATE: 33-MAY-1994
CLASSIFICATION NUMBER: 36,00
REFERENCE/DOCKET NUMBER: MIV-029.01
TELEPHONE: (617) 832-1000
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TWATEN TO THE CHARACTERISTICS:
LENGTH: 2624 base pairs
  REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-029CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 Archicarchiricherchic 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IlePheIlePheValPheIle 9
                                                                                                                                                                                                                                                                                                                                                                                                     00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                       1..2625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lineaı
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDREL CLLC
STREET: CLLC
-mv: Boston
                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
; LOCATION: 1...2
US-08-486-663A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-247-904B-7/c
                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                         score:
```

```
CORAL
STREET: One
CITY: Boston
STATE: MA
COUNTRY: USA
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT: INFORMATION:
NAME: Vincent, Matthew P.
RESTRANCE/DOCKET NUMBER: 36,709
RESTRANCE/DOCKET NUMBER: 36,709
TELEFAX: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: AARACTERISTICS:
"AARACTERISTICS:
"AARACTERIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20. Application US/08767942A
Patent No. 6068982
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONUCATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSE:
CORRESPONDENCE ADDRES
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-08-247-904B-7 (1-2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 Arcricarcrirercricare 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IlePhellePheValPhelle 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
12.07%
                                                                                                                            100.00%
100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.,2622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                 Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: CDS
; LOCATION: 1..2
US-08-767-942A-20
```

Tue Aug 17 16:21:37 2004

දු පු

Search completed: August 16, 2004, 01:14:03 Job time : 68 secs

Lhis Page Blank (uspto)

Appli Appli Appli Appli Appli Appli

```
Sequence 48, Appl Sequence 9815, Appl Sequence 92870, Appl Sequence 9125, Appl Sequence 50629, Appl Sequence 13177, Appl Sequence 13177, Appl Sequence 13177, Appl Sequence 13267, Appl Sequence 13267, Appl Sequence 1105, Appl Sequence 1105, Appl Sequence 6117, Appl Sequence 1105, Appl Sequence 20, Appl Sequence 20, Appl Sequence 1054, Appl Sequence 10544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 148, App
Sequence 36128, A
Sequence 60602, A
Sequence 61489, A
Sequence 61489, A
Sequence 61688, A
Sequence 61688, A
Sequence 61688, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 304, App
Sequence 32017, A
                                               Sequence Sequence Sequence S
                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VESTOLIC IN VESTOR OF START IS SEQUENCE 15, Application US/10079754A; Publication NO. US2020164625A1; Sequence 15, Application NO. US2020164625A1; Sequence 15, Application NO. US2020164625A1; SEQUENCE INFORMATION: Matthew APPLICANT: Glenn, Matthew APPLICANT: Molenaar, Adrian J. APPLICANT: Davis, Stephen R. TITLE OF INVENTION: Compositions Isolated from Bovine TITLE OF INVENTION: Compositions isolated from Bovine TITLE OF INVENTION: Mammary Gland and Methods for Their USE FILE REPERBENCE: 1100.1.068; CURRENT APPLICATION NUMBER: US 09/699,146; PRIOR PAPLICATION NUMBER: US 09/699,146; PRIOR PELING DATE: 2000-10-27; PRIOR PELING DATE: 2000-08-22; PRIOR APPLICATION NUMBER: US 09/644,190; PRIOR PELING DATE: 2000-08-22; PRIOR APPLICATION NUMBER: US 60,150,330; PRIOR FILING DATE: 1000-08-23; NUMBER OF SEQ ID NOS: 15
ALIGNMENTS
      υυυυ
                                                                                                                                                                                                                       υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
-MODEL=frame+ p2n.model -DEV=Xlh
-Q=/CGR2 1/USFO_SPO01/US10079754/runat_06082004_181357_29554/app_query.fasta_1.199
-Q=/CGR2 1/USFO_SPO01/US10079754/runat_06082004_181357_29554/app_query.fasta_1.199
-LOB=Published_Applications_NA -QFMT=fastap -SUPFIX=rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -ENN=-1 -MATR.X=0190
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR_NN=1
-ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10079754 @CGN 1 1.480 @runat_06082004 181357_29954
-NCPIG= -LOCHUS -NO MAAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOTT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
                                                                                                                                                               (without alignments)
872.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                     MKIFIFVFIMALILAMIRAD.......OQYQPYQRYPLNYPPAYPFP
                                                                                                                                      August 16, 2004, 01:12:59; Search time 326 Seconds
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                             OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           3225727 seqs, 2453303834 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                Xgapext 60.0
Ygapext 60.0
Fgapext 7.0
Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
                                                                                                                                                                                                                   US-10-079-754A-10
58
1 MKIFIFVFIMALILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                            OLIGO
Xgapop 60.0 , X
Ygapop 60.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size:
```

Result

Searched:

Run on:

```
58.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-1
                US-10-079-754A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                             104 TCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAACATCATAGAGGGATATTTTCAACAA 163
                                                                                                                                                                                                                                                                                                            44 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 103
                                                                                                                                                                                                                                                                                       1 MetrysllephellepheValPhelleMetAlaLeulleLeuAlaMetlleArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                       21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                           164 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                           41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 200, Application US/10079623

Sequence 200, Application US/10079623

Sublication No. US20020169302A1

GENERAL INFORMATION:

APPLICANT: Harvikala, 11kka J.

APPLICANT: Glenn, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Molenaar, Adrian J.

ITLE OF INVENTION: Compositions isolated from bovine

ITLE OF INVENTION: mammary gland and methods for their use.

FILE REPREBENCE: 11000.1044c3

CURRENT APPLICATION NUMBER: US/10/079,623

CURRENT FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 370

SEQ ID NO 200

SEQ ID NO 200

LENGTH: 267
                                                                                                                                  267
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-10-079-623-200 (1-267)
                                                                                                                                                                                                                                                       US-10-079-754A-10 (1-58) x US-10-079-754A-15 (1-267)
; SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15 LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.016-54
58.00
100.00%
100.00%
                                                                                                                                    9.01e-54
58.00
100.00%
100.00%
                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Bovine
                                                     TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-079-623-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-623-200
                                                                                     US-10-079-754A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                         Pred. No.:
                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
Sequence 1, Application US/10079754A

Publication No. US20020164625A1

Sequence 1, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Mammary Gland and Methods for Their Use TITLE OF INVENTION: Mammary Gland and Methods for Their Use FILE REFERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19

FRIOR PILING DATE: 2000-10-27

FRIOR PILING DATE: 2000-08-22

FRIOR PILING DATE: 2000-08-22

FRIOR PILING DATE: 2000-08-23

NUMBER OF SEC ID NOS: 15

SEC ID NO 1

LENGTH: 505

FRIOR LENGTH: 505

FRIOR LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10079754A; Sequence 4, Application No. US20020164625A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Marthew
APPLICANT: Glenn, Marthew
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated for Their Use
FILE REPERENCE: 11000-1068
CURRENT APPLICATION WUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR PEPLICATION NUMBER: US 09/699,146
PRIOR PELLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/64,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR PELLING DATE: 1999-10-29
PRIOR PELLING DATE: 1900-008-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-10-079-754A-1 (1-505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
```

```
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                       ò
                                                                                                            g
                                                                                                                                                                          à
                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetLysllePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2. Application US/10079754A

Sequence 2. Application US/10079754A

Sublication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn. Matthew

APPLICANT: Glenn. Matthew

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REPERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR FILING DATE: 2002-02-19

PRIOR PRIOR PELICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR FILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 00,150,330

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1090-08-22

NUMBER OF SEQ ID NOS: 15

LENGARD: 1500-08-23

NUMBER OF SEQ ID NOS: 15

LENGARD: 1000-08-22

LENGARD: 1000-08-22

LENGARD: 1000-08-22

LENGARD: 1000-08-22

LENGARD: 1000-08-22

PRIOR FILING DATE: 1000-08-23

NUMBER OF SEQ ID NOS: 15

LENGARD: 1000-08-22

LENGARD: 1000-08-22

LENGARD: 1000-08-22

PRIOR FILING DATE: 1000-08-23

NUMBER OF SEQ ID NOS: 15

LENGARD: 1000-08-22

LENGARD: 1000-08-22

PRIOR FILING DATE: 1000-08-23

NUMBER OF SEQ ID NOS: 15

LENGARD: 1000-08-22

LENGARD: 1000-08-23

LENGARD: 1000-08-23

PRIOR FILING DATE: 1000-08-23
                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-10-079-754A-2 (1-585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-079-754A-10 (1-58) x US-10-079-754A-4 (1-604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.03e-46
51.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                            1.97e-53
58.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
```

PhelleMetalaLeulleLeualaMetlleArgAlaAspSerSerGluGluLySArgHis 27

```
230 AGGAAACGGAAAAAAAACATCATAGAAGATATTTTTCAACAATACCAGCCATATCAACGATAT 289
170 ITCATTATGGCICTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCAC 229
                                                                                           28 ArglysArglysHisHisHisArgGlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCOMPATION:

GENERAL INCOMPATION:

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

TITLE OF INVENTION: Compositions isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REPERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 00.162,701

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

FANCE FASTER FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10079754A
; Sequence 3, Application US/10079754A
; Publication No. US20020164625A1
; GABERAL INFORMATION:
    APPLICANT: Grigor, Murray R.
    APPLICANT: Molenar, Adrian J.
    TITLE OF INVENTION: Compositions Isolated from Bovine
    TITLE OF INVENTION: Mammary Gland and Methods for Their Use
    FILE REPERENCE: 11000.1068
    CURRENT PAPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 rcarcraaadadaacgrcacagaaacggaaaaaaacarcar 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 SerSerGluGluLysArgHisArgLysArgLysLysHisHis 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 5
0 0
0 0
0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-10 (1-58) x US-10-079-754A-6 (1-525)
                                                                                                                                                                                                                                                                                                                                                                           290 ccácraaarrarccrccrccrarrccarrrccr 322
                                                                                                                                                                                                                                                                                   48 ProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-079-754A-6
'Sequence 6, Application US/10079754A
'Sublication No. US20020164625A1
'GENERAL INFORMATION'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e-27
34.00
100.00$
100.00$
58.62$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-754A-6
```

```
Sequence 48, Application US/09812350

Bublication No. US202020053097A1

GENERAL INFORMATION:
APPLICANT: Lindquist, Susan
APPLICANT: Variation
APPLICANTON VUMBER: US 60/190, 769
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 60/190, 769
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH APPLICANTON
APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLICANTON APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-995-8815
Sequence 8815, Application US/09918995
Sequence 8815, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PELLING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7726
9
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
8
0
0
```

8

```
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 56029
LENGTH: 808
                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT RELIGHTON NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 8118
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CTHER INFORMATION: Clone ID: PAT_MRT4530_57980C.1 US-10-437-963-56029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-10 (1-58) x US-09-918-995-8118 (1-464)
           US-10-079-754A-10 (1-58) x US-09-918-995-8225 (1-390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                      137 Argectricartriceceardare 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 Argechricarrirecedardard 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 MetAlaLeuIleLeuAlaMetIle 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 56029, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                         10 MetalaLeuIleLeuAlaMetIle 17
                                                                                                                                                                                       Sequence 8118, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NAME/KEY: misc_feature
| LOCATION: (1) ... (464)
| CTHER INFORMATION: n = A,T,C or G
US-09-918-995-8118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bulkharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
13.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-56029/c
                                                                                                                                                   RESULT 13
US-09-918-995-8118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: And Vibua
APPLICANT: About Vibua
APPLICANT: Cac Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERQ ID NO 92870
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE REPERRNCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/218,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE FELSEQ for Windows Version 3.0
SEQ ID NO 8225
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-079-754A-10 (1-58) x US-10-424-599-92870 (1-339)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRATURE:
OTHER INFORMATION: Clone ID: PAT MRT3847_54877C.1
                                        US-10-079-754A-10 (1-58) x US-09-918-995-8815 (1-181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 ATGATCCGCCCAGACTCGAGTGAG 202
                                                                                                                                92 Ardecrirdarrirdeceardard 115
                                                                                                                                                                                                                    Sequence 92870, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 MetileArgAlaAspSerSerGlu 23
                                                                                        10 MetAlaLeuIleLeuAlaMetIle 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-918-995-8225
; Sequence 8225, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3
8.00
100.00%
100.00%
113.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.5
8.00
100.00%
100.00%
13.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                           RESULT 11
US-10-424-599-92870/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-92870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-995-8225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
RESULT 15
US-10-198-846-5963/C
SGUENCE 5963, Application US/10198846
Publication No. US2003009974A1
Publication No. US2003009974A1
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lilla, James
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: TORY IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: UNMERR: US/10/198,846
CURRENT FILLING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PELICATION NUMBER: 60/306,220
PRIOR PELICATION NUMBER: 60/306,220
PRIOR SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5963
LENGTH: BNA
ORGANISM: Homo sapiens
FAATURE:
NAME/KEY: misc feature
LOCATION: 768, 712, 496, 541, 543, 646, 649, 653, 711, 730, 742, 764, 10-2071ION: 768, 779, 781, 785, 800, 804, 809, 811, 821, 823, 829, 10-2071ER INFORMATION: n = A,T,C or G
US-10-198-846-5963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 4 7 0
0 0 0 0 0
               880000
             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                            US-10-079-754A-10 (1-58) x US-10-437-963-56029 (1-808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                11 AlaLeuIleLeuAlaMetIleArg 18
                                                                                                                                                                                                      90 GCCCTCATCTTGGCTATGATCAGG 67
                                                  100.00%
100.00%
13.79%
                                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                     Query Match:
DB:
                                    Score:
                                                                                                                                                                                  à
```

US-10-079-754A-10 (1-58) x US-10-198-846-5963 (1-870)

100.00% 100.00% 13.79%

Percent Similarity: Best Local Similarity: Query Match: DB:

Score:

Search completed: August 16, 2004, 02:01:13 Job time : 329 secs

Sequence:

:uo

Run

Searched:

```
Sequence 20065, A Sequence 13, Appl Sequence 13, Appl Sequence 7127, App Sequence 9144, App Sequence 8, Appli Sequence 2, Appli
                                Sequence
Sequence
Sequence
                                                                                                                                          Sequence (Sequence (Sequen
                                                                                                                                                                                           Sequence Sequence S
                                                                                                                                                                                                                                                 Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                     Sequence Sequence Sequence
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1

US-08-415-818-12

US-08-415-818-12

Sequence 12, Application US/08415818
Fatent No. 5621079
Fatent No. 5621079
Fatent No. 5621079
FAPLICANT: Cascieri, Margaret A. APPLICANT: Linemeyer, David L. APPLICANT: Shiso, Lin-Lin
APPLICANT: Tan, Carina P. APPLICANT: Tan, Carina P. APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR NUMBER OF SCUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Mary A. Appollina
STREET: NO. Box 2000, 126 E. Lincoln Ave. CITY: Rahway
STREET: NO. Box 2000, 126 E. Lincoln Ave. CITY: Rahway
COUNTRY: USA
ZIP: 07065
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALCATION DATA:
APPLICATION NUMBER: US/08/415,818
FILING DATE: PALCATION NUMBER: US/08/415,818
FILING DATE: O3-FEB-1995
ATPORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 08/383,746
FILING DATE: O3-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITING NUMBER: 34,087
REGISTRATION NUMBER: 34,087
                            O
                                                                                                                                0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-0=/cgn2 1/U28PTO spool p/USI0079754/runat_06082004_180756_1728/app_query.fasta_1.775
-0=/cgn2_1/USPTO spool p/USI0079754/runat_06082004_180756_1_1-LOOPCL=0
-DB=1squed_Patenfs_AA_OFMT=6astan -SUFFIX=rai -MINMATCR=0.1_-LOOPCL=0
-LOOPEXT=0 -UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-9Ct -THR MINED-0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPPIZE=500 -MINILEN=0 -MXLEN=20000000
-USER=USIO079754 @cCN 1 1.27 @runat -0608202E=500 -MINILEN=0 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Appl
Sequence 12, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 19816, Ap
Sequence 19816, Ap
Sequence 5672, Ap
Sequence 25, Appli
Sequence 2, Appli
                                                                                                                              August 6, 2004, 17:10:01; Search time 22 Seconds (without alignments) 2834.735 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                               US-10-079-754A-4
1029
1 gaagtattttcagttctata......tatcaagcataaaaaaaa 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
11. \G9Ta_6\pyodata_2\iaa\5A_COMB.pep:*
12. \G9Ta_6\pyodata_2\iaa\5B_COMB.pep:*
3: \G9Ta_6\pyodata_2\iaa\6A_COMB.pep:*
4: \G9Ta_6\pyodata_2\iaa\6B_COMB.pep:*
5: \G9Ta_6\pyodata_2\iaa\PyoTug_COMB.pep:*
6: \G9Ta_6\pyodata_2\iaa\PyoTug_COMB.pep:*
6: \G9Ta_6\pyodata_2\iaa\PyoTug_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-415-818-12

US-08-894-236-12

PCT-US96-01444-12

US-09-495-714C-4

US-09-495-714C-4

US-09-495-714C-6

US-09-495-714C-6

US-09-252-991A-19818

US-09-252-991A-19818

US-08-936-165A-395

US-08-107-53A-5672

US-08-159-340A-25

US-08-286-819A-25
                                                                                             OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370
370
1912
1912
1985
233
275
275
161
                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
```

Result

000000

3, Appl

Sequence Sequence Sequence Sequence

2, Appli 20066, A

227, Appl. 1, Appl. 5222, Ap 6, Appl. 6, Appl. 6, Appl. 6, Appl. 112, Appl. 112, Appl. 112, Appl. 112, Appl. 113, Appl. 114, Appl. 114, Appl. 115, Appl. 116, Appl. 117, Appl.

Sequence

Sequence

```
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Stader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RENUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORKEY/AGENT INFORMATION:
NAME: APPOILINA, MARY A.
REGISTRATION NUMBER: 34,087
REFRENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19390Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.00
35.51%
22.90%
7.23%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                              STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                          07065
                                                                                                                                                                                                                                     STATE: NJ
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-894-236-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 MetAspHisTrpllePheGlyAspThrMetCysArgLeuThrSerTyrValGlnSerVal 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 -----TTATTCATTTGAAAGATGGTTTTCAACACAGAAAGAGTAGGAAAAATC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 ATGGTAAGTGACAGAGAAAGAAAGTAGAA-----ACCAATTACATAGTTCAGAGACTA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GIGAAAAAICICICIAAICAIGICCIGIAGIIACIAAGCAGCAIT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 TTAAGGAAATGGATACGCAGGAGGATAATTTAGTGG----ATATCGTTGATATGGCTGGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 TIGITGAAAATAICCICTAIGAIGITTITICCGITITCCIGIGACGITICTCTICAGAIGA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 ATCAGCTCTAATCATGGCTAGGATGAGAGC---CATAATGAAGACAAAGATAAAGATCTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TGGTGGAGTCCAGTCATGAAAGATGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 TyrThrHisGlnValAlaCysValGluAsnTrp-----ProSerLysLysAspArgLeu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||
79 SerLeuSerAspThrLeuValCysValMetCysIleHisPheThrIleIleTyrThrLeu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGATGCTTCAGGAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ii:
139 ValAsnProArgGlyTrpLysProSerValThrHisAlaTyr---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TTATTATGTTTTAAAATATTGATATTTGATTTCCAAGTATGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 PheileLeulleCys---TyrLeuLysIleValileCysLeu 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 TICATITICITATIACATIACATCAGITATGAGATCTTATTA 19
                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-4 (1-604) x US-08-415-818-12 (1-370)
                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08894236
Patent No. 5939263
GENERAL INFORMATION:
APPLICANT: Cascieri, Margaret A.
                                                         TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNES; single
    REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
                                                                                                                                                                                                                                                                          0.892
75.00
35.51$
22.90$
                                                                                                                                                                           TOPOLOGY: linear ADLECULE TYPE: protein US-08-415-818-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 TCA-----
                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-894-236-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153
                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
```

```
511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 -----TTATTCATTTGAAAGATGGTTTTCAACACAGAAAAGAGTAGGAAAAATC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 ATT------GTGAAAATCTCTCTAATCATGTCTGTAGTTACTAAGCAGCATT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 ATGGTAAGTGACAGAAAAAAAAAGAAGTAGAA-----ACCAATTACATAGTTCAGAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 ileilePheLysLysGlnArgLysAlaGlnAsnPheThrSerIleLeuIleAlaAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 MetAspHisTrpllePheGlyAspThrMetCysArgLeuThrSerTyrValGlnSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 TCA------TTATTATGTTTTAAAATATTGATTTGATTCCAAGTATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370
27
70
68
13
                                                                                                                      COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-4 (1-604) x US-08-894-236-12 (1-370)
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/894,236
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-F82-1995
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
```

; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein PCT-US96-01444-12	-10-079-754A	Qy 564 ATGGIAAGIGACACAGAAAAAAGAAAGAAAGAAAGAAAGAAA	Oy 510 TCATTATTATGTTTTA	Qy 462 TGCAACTACDb 99 MetAspHisTrpllePheGlyAspThrM	Qy 429TATICALITGAAAGAIGG	119	Oy 5/8 ATT	Qy 330 TTAAGGAAATGGATACGCAGGAGGATAA	Db 153	OY 273 TIGITGAAARATCCTCTATGAIGTTTT	162	OY 213 ATCAGCICTAAICALGGCIAGGAALAACA DD 177ASpGluP		::: Db 190 TyrThrHisGlnValAlaCysValGluA		8 0	Db 224 PhelleLeulleCysTyrLeuLysl	RESULT 4 US-09-495-714C-2 Sequence 2, Application US/09495714C Patent No. 6670465 GENERAL INFORMATION: APPLICANT: University Technologies Intering APPLICANT: University Technologies Intering TITLE OF INVENTION: RETINAL CALCIUM CHAPTION: FILE REFERENCE: 45499.4 (formerly 45074); CURRENT APPLICATION NUMBER: US/09/495,770 CURRENT APPLICATION NUMBER: US/09/495,780 NUMBER OF SEQ ID NOS: 138 SOFTWARE: Patentin version 3.1 SEQ ID NO 2 LENGTH: 1912
		Qy 156 CATATT	OY 120 CTGATGCTTCAGGAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCC 61	Oy 60 TICAITIGIAATIACAICAGITAIGAGAICITAITA 19	RESULT 3	e 12, Ap	; APPLICANT: Cascieri, Margaret A. ; APPLICANT: Linemeyer, David L. ; APPLICANT: MacNeil. Douglas J.	; APPLICANT: Shiao, Lin-Lin; APPLICANT: Strader, Catherine D.	rina P. g, David H.	; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR ; NUMBER OF SEQUENCES: 14) CORKENSORDER, AND MESSAS A APPOLITINA STREET: P.O. BOX 2000, 126 E. Lincoln Ave.	; CITY: Rahway ; STATE: NJ COTAMIDY: NJ	065 EADABLE FORM:	, MEDIUM TYPE: Floppy disk , COMPUTER: IBM PC compatible	; OPERATING SYSTEM: PC-DUS/NS-LUS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: PCT/US96/01444 ; FILING DATE:	; CLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/383,746	FILING DATE: 03-FEB-1995 PRIOR APPLICATION DATA: 08/415,818 APPLICATION NUMBER: 08/415,818 FILING DATE: 03-APR-1995 ATTORNEY-YGENTI INFORMATION: NAME: APPOILINA, MALY A. REGISTRATION NUMBER: 34,087 REPERENCE/DOCKET NUMBER: 19390Y TELEPHONE: 908-594-3462 ITELEPHONE: 908-594-3462 ITELEPAX: 908-594-3462 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acids TYPE: amino acid

```
ATTTAGTGG---ATATCGTTGATATGGCTGGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TTGACTGATTTTTTTTTTTTT 430
                                                                                                                                                                                         GTTTTCAACACACAGAAAGAGTAGGAAAAATC 379
                                                                                                                                                                                                                                          TCTAATCATGTCCTGTAGTTACTAAGCAGCATT 331
                                                                                                                                                                                                                                                                                    ValThrHisAlaTyr------152
                                                                                                                                                                                                                                                                                                                                                 TITICCGITICCIGIGACGITICTCTTCAGAIGA 214
                                                                                                                                                                                                                                                                                                                                                                  PAGC---CATAATGAAGACAAAGATAAAGATCTT 157
                                                                                                                                                                                                                                                                                                                                                                                                              ::: |||
| ISInTyrPheValProLeu-------Gly 223
                                                                                           GAA-----ACCAATTACATAGTTCAGAGACTA 511
                                                                                                                                   AAAATATTGATATTTGATTCCAAGTATGTGTTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAACTGCTGTTTTAAATACCTTGAAATCC 61
                                                                                                                                                    ::: |||
MetCysIleHisPheThrIleIleTyrThrLeu 98
                                                                                                       iternational Inc.
HANNEL (ALFHA) 1F-SUBUNIT GENE
74.6)
,714C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATGAGATCTTATTA 19
370
49
27
70
70
68
ength:
atches:
onservative:
ismatches:
ndels:
aps:
                                                                         -12 (1-370)
```

```
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                       -09-495-714C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-495-714C-6
                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                   g
                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                       g
                                                                          ò
                                                                                                                                     à
                                                                                                                                                              QQ
                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                           249 TITITITCGGTTTCCTGTGACGTTTCTCTTCAGATGAATCAGCTCTAATCATGGCTAGGAT 190
                                                                                                                                                                                                                                                                                                                                                                                                                            ::::::||| :::
| | | | :::::|
521 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 640
                                                                                                                                                                                                                   369 AATCTCTCTAATCATGTCCTGTAGTTACTAAGCAGCATTTTAAGGAAATGGATACGCAGG 310
                                                                                                                                                                                                                                  612 LeuPheGlyGlyLysPheAsnPhe-----Asp 620
                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGCCATAATGAAGACAAAGATAAAGAT--------CTTCATATTTGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AGGATAATTTAGTGGATATCGTTGATATGGCTGGTATTGTTGAAAATATCCTCTATGATG 250
                                                                                                                                                                                                                                                                                                  :::::: |||
594 LeuLeuLeu-----LeuLeuPheLeuPheIleIleIlePheSerLeuLeuGlyMetGln 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AATCTCTCTAATCATGTCCTGTAGTTACTAAGCAGCATTTTAAGGAAATGGATACGCAGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||||||||| ||| ||| 641 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerlleAlaSer 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 GAGATGITCTITGCTAGAAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09495714C

Patent No. 6670465

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) IF-SUBUNIT GENE
FILE REFERENCE: 45499.4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin version 3.1
LENGTH: 1977
                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                       US-10-079-754A-4 (1-604) x US-09-495-714C-2 (1-1912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-4 (1-604) x US-09-495-714C-4 (1-1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 GlyAsnTyrileLeuLeuAsnValPheLeu 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 TGTAATTACATCAGTTATGAGATCTTATTA 19
                                                                                                                                                       Gaps:
                                                                             1.94
73.50
42.31$
24.62$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.50
42.31%
24.62%
7.09%
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-495-714C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-495-714C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
249 ITITITICCGITICCTGIGACGITICICTICAGAIGAAICAGCICTAAICAGGIAGGAI 190
                                                                                                                                                                                                   -TGGAGTCCAGTCATGAAGATGAAATTCTGATGCTTCAG 109
                                                                                                                                                                                                                                                                                                                               706 GInIleLeuThrGlyGluAspTrpAsnValValMetTyrAspGlyIleMetAlaTyrGly 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AATCTCTCTAATCATGTGTCCTGTAGTTACTAAGCAGGATTTTAAGGAAAATGGATACGCAGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...iiiiiiii iii
641 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerIleAlaSer 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 TITITICGETITCCTGTGACGTTTCTCTTCAGATGAATCAGCTCTAATCATGGCTAGGAJ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 GAGAGCCATAATGAAGACAAAGATAAAGAT-------CTTCATATTGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::::::||| :::
686 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 GlnileLeuThrGlyGluAspTrpAsnValWalMetTyrAspGlyIleMetAlaTyrGly 725
309 AGGATAATITAGIGGATAICGIIGAIAIGGCIGGIAIIGIIGAAAAIAICCICIAIGAIG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                 726 GlyProPhePheProGlyMetLeuValCysIleTyrPheIleIleLeuPheIleCys--- 744
                                                                                                                                                                                                                                                                                                                                                                                                    108 GAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AGGATAATTTAGTGGATATCGTTGATATGGCTGGTATTGTTGAAAATATCCTCTATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University Technologies International Inc.
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
FILE REPERENCE: 4599-4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1985
32
23
24
46
6
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-4 (1-604) x US-09-495-714C-6 (1-1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 IGTAATTACATCAGTTATGAGATCTTATTA 19
                                                                                                                                                      677 LeuPheGlyGlyLysPheAsnPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09495714C Patent No. 6670465 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 LeupheGlyGlyLysPheAsnPhe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.59
72.50
42.31%
24.62%
6.99%
```

```
|||||||||:::
|184 AspAsnLysLeuAspValvalGlnArgAlaLeuGlyLeu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AGTCAAGTAGTTGCACACACATACTTGGAATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275
24
20
52
67
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-4 (1-604) x US-09-252-991A-19818 (1-275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCAAATATGAAGATCTTTATCTTTGTCTTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OKGANISM: Pseudomonas aeruginosa
US-09-252-991A-19818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 -----
178 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::: :::
ThrPheLeuSerGluGluArgLeuLysLeuGlnAlaProLeuValIleArgLeuGlyGln 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: :::||| :::||| | || ISBGIUGIUASNITHTGIYILEGIUProASN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 IleThrGluSerGlyGlnTrpAsn-MetSerGlyAsnAspValCysAsnPheArgValle 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAG 364
                                   26 GlyProPhePheProGlyMetLeuValCysValTyrPheIleIleLeuPheIleCys--- 744
      GAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 AGAITITICACAAIGAITITICCIACICITICIGITGIAAAACCAICITICAAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --AATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
25
20
32
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                        Sequence 176, Application US/09489847
Patent No. 6476195
GRENEAL INFORMATION
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFRENCE: PO20191
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
GEALLER FILEND DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER PILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER RILING DATE: 1998-08-05
EARLIER RILING DATE: 1998-08-06
EARLIER RILING DATE: 1998-08-06
SARLIER RILING DATE: 1998-08-06
SARLIER RILING DATE: 1998-08-06
SARLIER FILING DATE: 1998-08-06
SARLIER FILING DATE: 1998-08-06
SARLIER PILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-4 (1-604) x US-09-489-847-176 (1-233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (233)
COTATE NIFORMATION: Xaa equals stop translation
US-09-489-847-176
                                                                                                                  485 ATCAATATTTAAAACAT--------
                                                                                          TGTAATTACATCAGTTATGAGATCTTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.34
70.00
43.27%
24.04%
6.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICITITICIC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                               -09-489-847-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
           108
                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                        δ
```

```
## KESULO.

## Sequence 19818, Application US/0925291A

## PPLICANT: Marc J. Rubenfield et al.

## APPLICANT: Marc J. Rubenfield et al.

## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

## TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

## CURRENT APPLICATION NUMBER: US/09/252,991A

## CURRENT FILING DATE: 1998-02-18

## PRIOR PLILING DATE: 1998-02-18

## PRIOR PLILING DATE: 1998-07-27

## NUMBER OF SEQ ID NOS: 33142

## SEQ ID NO 19918

## SEQ ID NO 19918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 CAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||:::|||:::|||||:::
30 ProProAspMetArgIlePheLeuProAlaLeuLeuAlaTrpSerSerThrArgThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 ArgProArgProAlaAlaValIleAlaHisIleSerProAlaAlaProAlaProThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::|||||| :::
70 SerThrSerValLeuAlaThrValProLeuArgSerSerGluThrAlaArg1leLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 ------CACAGGAAACGGAAAAAAAAAAAATATTTTCAACAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 ProAspProCysMetIleProLeuLysTyrLeuGlnAlaTyrProAlaSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 GCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAATGAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-936-165A-395
```

```
RESULT 10
US-09-107-512A-5672
US-09-107-512A-5672
Sequence 5672, Application US/09107532A
Sequence 5672, Application US/09107532A
GENERAL INFORMATION:
APPLICANT: LYPIN A Doucette-Stamm and David Bush
APPLICANT: LYPIN A DOUCETIC ACID ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION:
                                                    |||:::
-----PhelleAlaIl 111
                             105 ATGITCTTTGCTAGAAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTTTGT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482
188
188
144
174
174
174
174
174
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-4 (1-604) x US-09-107-532A-5672 (1-482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 AAGAAAGTAGAAACCAATTACATAGTTCAGAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Un-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1497
ATTORNEY/AGENT INFORMATION:
NAME: AATHAILO, PREMISE: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                              111 eLeuThrLeuThrMetTrpSerGluTyrArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...482
SEQUENCE DESCRIPTION: SEQ ID NO: 5672:
                                                                                                             45 AATTACATCAGTTATGAGATCTTATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 482 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5672:
                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.00
43.54%
21.09%
6.56%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-107-532A-5672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
90
                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                     쉱
                                                                                                             ò
                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTTCAGATGAATCAGCTCTAATCATGGCTAGGATGAGAGCCATAATGAAGACAAAGAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AAAGATCTTCATATTTGGTGGAGTCCAGTCATGAAAGATGAAATTCTGATGCTTCAGGAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ArgHisAlaLeuIleLeuPheValAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ileTrpSerAsnPheIleGluMetGlySerMetMetLeuLeuProMetSerMetLeuPhe 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 ATATGGCTGGTATTGTTGAAAAAATATCCTCTATGATGTTTTTTTCCGTTTTCCTGTGACGTTT
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SQUENCES: 534
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OURPULEAR: LEN. COMPACTALL
OPERATING SYSTEM: DOS
SOFTWARE: | FRSESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAME: Ginmi, Edward R
REGISTRATION NUMBER: 98,891
REGISTRATION NUMBER: 980549
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-4 (1-604) x US-08-936-165A-395 (1-273)
                                                                                                                                                                                                                                                                                                                                                  SSEE: SmithKline Beecham Corporation
7: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 LeupheGlyArgMetLeuSerArgHisGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
              Application US/08936165A
                                                                                          Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysArgValHis------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395:
                                                                                                                                                                                                                                    Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: ......
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIDE
Sequence 395, Applica...
Patent No. 6348582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.66%
25.27%
6.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 705
CITY: King
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-936-165A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
::: :::::: |||||| :::|||:::|
167 GlnAsnLeuLysPheAsnTyrLysMetGlnGlnTyrTyrPheValPheThrLeuIlePhe 186
```

```
238
                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                               242 LysAsnIleArgArgLeuLeuValSerSerPheLeuPheIleTyrAsnValAsnProPhe 261
AACTACTIGACIGATITITITITITITITITITITITITITIGAAAGAIGGITITICAACACA 400
                                                                                                        399 ACAGAAAGAGTA-----GGAAAAATCATTGTG------AAAAATCTCTCTAAATCAT 355
                                                                                                                                                                                                                                                                                     -----AGGAAATGGATACGCAGGAGATAATTTAGTGGATATCGTTGATATGCCTG 277
                                                                                                                                                                                                                                                                                                                                                                                  262 AsnValSerArgTyrTyrIleSerTyrValValIleLeuPheMetLeuIlePhePheThr
                        276 GIAITGTIGAAAATAICCICIAIG----------AIGIITITICCGIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOSITIONS
                                                                                             |||| :::||||:::
207 AsnLeulleThrAsnSerSerLeuTyrLeuIlePhe----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,340A
FILING DATE: 24-NOV-1993
                                                                                                                                                                                                                  GTC------CTGTAGTTACTAAGCAGCATTTTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08159340A
Patent No. 556352
GENERAL INFORMATION:
APPLICANT: Hochstrasser, Mark
APPLICANT: Papa, Feroz
TITLE OF INVENTION: AND METHODS
ITLIE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARCD:112/HYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                 237 CCTGTGACGTTTCTCTTCAGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 proLeuleuasnPhephearg 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGIESTRATION UNURER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAK: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-159-340A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-159-340A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: T
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                    459
                                                                                                                                                                                                                  354
                                                                                                                                                                                                                                                                                       327
                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                    δ
                                                                                                    음
                                                                                                                                            ò
                                                                                                                                                                          g
                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                       à
```

926

9.1

```
GENERAL INFORMATION:

APPLICANT: ACTHERINE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
ANDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                    449
                                                                                                                                                                                                                                                                                                                                                                      469
                                                                                                                                                                                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                                                                                                                                                        489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531
                                                                                                                                                                                                  177
                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ATTATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAAGGTCACCAGGG
                                                                                                                                                                                                                                                                                                                                                                      yAsnSerPheArgIleAsnTyrProGluThrProHisLeuTrpLysAsnSerGluThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                            CCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 A------TGATTAGAGAGATTTTTCACAATGATTTTTCCT---ACTCTTTCTGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 nLeu------AsnMetAsnSerAsnGlyHisSerSerAlaThrSerThrIleGl
                                                                                                                                    CAGCAGITITICIAGCAAAGAACAICICCIGAAGCAICAGAAITIC-------AICITI
                                                                                                                                                                                                                       ---AACAATACCAGCCATATCAACGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| :::||||| ||| ||| 429 rLeuSerProAspProVallysG1
                                                                                                                                                                                                                                                                                                                                    ------AAAAACATCATAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 CAACACATACTTGGAATCAAATATCAATATTTTAAAACATAATAATGATAGTCTC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AsnAsnAspSerLeu 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
   225
225
101
101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: PARENTE REAGENER RELEGATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
                   Conservative:
Mismatches:
                                                                                                   US-10-079-754A-4 (1-604) x US-08-159-340A-2 (1-926)
                                                                                                                                                                                                      CATGACTGGACTCCACCAAATATGAAG-----
   Matches:
                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 nProSerCysLeuSerLeuSer---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08286819A
Patent No. 5871910
                                                                                                                                                                                                                                                                                                                                        238 AAACGGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | | :::|| | | | | 500 rAlaThrProLysLeuGlnArg
67.50
39.11$
26.82$
6.56$
                                                                                                                                                                                                                                                                                                                                                                                                          TATTTC--
                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 eAsn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-286-819A-25
                                                                                                                                     82
                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                          449
                                                                                                                                                                                                                                                                                                                                                                                                          262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295
                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                     ò
                                                                                                                                                                      a
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                          \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
91 TCTAGCAAAGAACATCTCCTGAAGCATCAGAATTTCATCTTTCATGACTGGACTCCACCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ATAACTGATGTAATTACAAAACAAATGAAGGATTTCAAGGTATTTAAACACAGCAGTTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AATAIGAAGAICTITATCTITGTCTTCATTAIGGCTCTCATCTAGCCAIGAIT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
21
8
18
11
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-4 (1-604) x US-08-980-357-25 (1-161)
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/US/200,337
FILING DATE: US/US/200,337
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 05-BEC-1993
PRIOR APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
RIGH APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 39-OCT-1991
PRIOR APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 31-OCT-1991
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 31-OCT-1990
ATTORNEY/ABRI INFORMATION:
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60, Application US/09393634
Patent No. 6558910
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zuker, Charles S. APPLICANT: Adler, Jon Elliot APPLICANT: Ryba, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.50
50.00%
36.21%
6.46%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-980-357-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                              Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
  CITY: Arl
STATE: Vi
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-393-634-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/08980357

Sequence 25, Application US/08980357

Patent No. 601384

Patent No. 601384

APPLICANT: ARTHUR, MICHEL

APPLICANT: DUKTN-AMLEN, STUVIE

APPLICANT: COURVALIN PARRICE

TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 54

CORRESPONDENCE SDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 ileThrAspValileThrAsnThrValGlyGlyPheLeuGlyLeuLysLeuTyrGlyLeu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTAGCAAAGAACATCTCCTGAAGCATCAGAATTTCATCTTTCATGACTGGACTCCACCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 ATAACTGATGTAATTACAAAAACAAATGAAGGATTTCAAGGTATTTAAACACAGCAGTTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 SerAsn------LysHisMetAsnGlnLysLysLeuAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-4 (1-604) x US-08-286-819A-25 (1-161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPAX: 248855 OPAT UR
INFORMATION FOR SEQ 1D NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                    APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1991
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1991
PRIOR APPLICATION DATA:
FILING DATE: 31-0CT-1990
FILING DATE: 31-0CT-1990
CLASSIFICATION: 435
DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 161 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.32
66.50
50.00%
36.21%
6.46%
       FILING DATE: 05-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-286-819A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-980-357-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
```

σ

```
..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 TIGACTGATTTTTTTTTTTTTTTTTTTTTTTTGAAAGATGGTTTTTCAACACACAGAA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 AGAGTAGGAAAATCATTGTGAAAATCTCTCTAATCATGTCCTGTAGTTACTAAGCAGC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ATAATTTAGTGGATATCGTTGATATGGCTGGTATTGTTGAAAATATCCTCTATGATG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ------GlupheileileGlyAsnLeuGlyAsnSerPheileAlaLeuValAsnCys 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||-----AspTrpValLysGlyArgLysIleSerSerValAspArgIleLeuThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::
51 LeuAlalleSerArgIleSerLeuValTrpLeullePheGlySerTrpCysValSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 TTTTTTCCG-----TTTCCTGTGACGTTTCTCTTCAGATGAATCAGCTCT-----
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REPERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60
HUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Glevera, Jr., Juan G.
APPLICANT: Hogeveen, Ron C.
APPLICANT: Hogeveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: UECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
26
16
29
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-4 (1-604) x US-09-393-634-60 (1-317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IleLysSerIlePheThrPheValLeuIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 ATTTTAAGGAAATGGATACGCAGGAGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 219, Application US/09079030 Patent No. 6635623 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: human GR14
US-09-393-634-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.61
66.50
40.38%
25.00%
6.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 -----AATCAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||
91 ValileAsnHis 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-079-030-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
145 CCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---IleGlnAspGluileAsnThrilePheAsnAspTyrIle 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ProfyrvalPheLysLeuLeuLysGluAsnLeuCysLeuAsnLeuHisLysPheAsnGlu 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 ---CITICAAAIGAAIAAAACAAAGAAAAAAAAAATCAGICAAGIAGIIGCACAACACAIA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 GATCTCATAACTGATGTAATTACAAAACAAATGAAGGATTTCAAGGTATTTAAACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ITTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 CCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAATGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CAGITITICIAGCAAAGAACAICICCIGAAGCAICAGAAITITCAICITITCAIGACIGGACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TGTTGTGTTGAAAACCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 SerLeuLysThrThrGluValLeuArgAsnLeuGlnAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PheThrTyrLeuIleAsnTyr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396
34
26
48
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||::: :::::: ||||
144 ---GluAspAsnIleLysGluMetLys-----
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-4 (1-604) x US-09-079-030-219 (1-396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: MCMillian, Nabeela R.
REGISTATION NUMBER: P-43,363
REFERENCE DOCKET NUMBER: ARAG:003
TELECOMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEPHONE: 512/418-300
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 6, 2004, 17:16:03
Job time : 27 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 CTTGGAATCAAATATCAATATTTT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
Floppy disk
                                                                                                                                                                                                                                                                                                                                               LENGTH: 396 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 TCCTACTCTTTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6
66.00
35.71%
20.24%
6.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                         CLASSIFICATION:
  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-079-030-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
```

```
Sequence 6, Appli
Sequence 6, Appli
Sequence 246, Appli
Sequence 147146,
Sequence 103, App
Sequence 103, App
Sequence 103, App
Sequence 54218, A
Sequence 54218, A
Sequence 5291, Ap
Sequence 204, App
Sequence 19215, Sequence 19215,
Sequence 19215,
Sequence 19218, App
                                                                                                                                                                                                                                                                                                                                                                                                                                         176, App
154373,
156848,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131, App
53563, A
71761, A
159483,
                                                                                                                                                                                                                                                                                                                                                                      193953,
192104,
63502, A
7, Appli
192041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2232, Ap
Sequence 52793, A
Sequence 127400,
                                                                                                         Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 395, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148811,
                                                                                  Sequence 168
Sequence 19,
Sequence 6,
                                                                                                                       Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3
Sequence 3
Sequence 5
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                              Sequence
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Molemar, Adrian J.
APPLICANT: Marmary R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Marmary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
US-10-437-963-148811
US-10-335-977-7067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 JS-10-079-754A-7
                                                                                                                                                                                                                                                                                                                                                         72.5
72.5
72.5
                                                                                                                                                                                                                                                                                                                                                                                                                            70.5
    316
316
316
315
14.5
1169
112
                                                                                                          74.5
73.5
73.5
73.5
                                                                                                                                                                                                                                                                                                         טטט
                                                                                                                                                                                                                                                                                                                                                                                                                                      August 6, 2004, 17:14:11; Search time 48.5 Seconds (without alignments) 7812.969 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                US-10-079-754A-4
1029
1 gaagtattttcagttctata......tatcaagcataaaaaaaa 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/2/Pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/Pubpaa/PCT_MBW_PUB.pep:*
3: /cgn2_6/ptodata/2/Pubpaa/PCT_MBW_PUB.pep:*
4: /cgn2_6/ptodata/2/Pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/Pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/Pubpaa/USO8_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/Pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/Pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/Pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/Pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/Pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/Pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/Pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/Pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/Pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/Pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/Pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/Pubpaa/USO0_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/Pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/Pubpaa/USO0_NEW_PUB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                      - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                         1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                       BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                          Scoring table:
                                                                      nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
                                                                                                Run on:
```

```
214 TCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ATGAAGATCTTTATCTTTGTCTTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                   1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp
                                                                                                                                                                                                                                                                                                        154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESULY 2

Sequence 10, Application US/10079754A

Sequence 10, Application US/10079754A

PUBLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions Isolated from Bovine

FILE REFERENCE: 11000.1069

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR PRILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARRE: FastSEQ for Windows Version 4.0

SSOFTWARRE: PAT

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
00000
                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-4 (1-604) x US-10-079-754A-10 (1-58)
                                                                                                                                                                                                                                                                  US-10-079-754A-4 (1-604) x US-10-079-754A-7 (1-58)
                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.13e-29
316.00
100.00$
100.00$
                                                                                                                                 4.13e-29
316.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-754A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                Alignment Scores:
                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
214 TCATCTGAAGAGAACGTCACAGGAAACGGAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AIGAAGAICITIAICITIGACITICATIAIGGCICTCAICCIAGCCAIGATIAGAGCTGAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCT 327
                                                                                     41 TyrGlnProfyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhebro 58
                                                                                                                         RESULT 3

US-10-079-754A-8

US-10-079-754A-8

Sequence 8, Application US/10079754A

Publication No. US202020164625A1

GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated for Their Use
TITLE OF INVENTION: Compositions Isolated for Their Use
FILE REFERENCE: 11000.1068
CURRENT FALLING DATE: 2002-02-19
PRIOR FILING DATE: 2000-10-27
PRIOR PRILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/10079754A

Sequence 12, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Grigor, Murray R.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REPERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-079-754A-4 (1-604) x US-10-079-754A-8 (1-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315.00
100.00%
98.28%
30.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Bovine
US-10-079-754A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-10-079-754A-12
                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Indels:

```
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-210-172-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: BOV
US-10-079-754A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                  δ
                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetLysilePheilePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SerSerGluGluLysArgHisArgLysArgLysLysLysHisValAspArgSerProGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 ------AGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCAC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 PheLeuLeulleGlnGlu-AspilePheAsnAsnThrSerHislleAsnAspileHis 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10079754A

Publication No. US2020164625A1

Publication No. US202020164625A1

Fublication No. US2020164625A1

APPLICANT: Glann, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Malenaar, Adrian J.

APPLICANT: Murray R.

TITLE OF INVENTION: Compositions Isolated from Bovine

FILE REFERENCE: 11000.1068

CURRENT FILING DATE: 2002-02-19

FRIOR PRICA APPLICATION NUMBER: US 69/699,146

FRIOR PRILING DATE: 2000-10-27

FRIOR FILING DATE: 2000-10-27

FRIOR PRILING DATE: 2000-08-22

FRIOR FILING DATE: 2000-08-22

FRIOR APPLICATION NUMBER: US 60,150,330

FRIOR FILING DATE: 1999-10-29

FRIOR FILING DATE: 1999-10-29

FRIOR PRILING DATE: 1999-10-29

FRIOR FILING DATE: 2000-08-22

FRIOR FILING DATE: 1008: 15

FRIOR FILING DATE: 1008-22

FRIOR FILING DATE: 1008-22

FRIOR FILING DATE: 1008-15

FRIOR FILING DATE: 1008-16

FRIOR FILING DATE: 1008-15

FRIOR FILING DATE: 1008-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 TCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAAAACATCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
17
17
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-4 (1-604) x US-10-079-754A-12 (1-59)
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR PLICATION NUMBER: US 60,162,701
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-23
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOUTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 59
TYPE: PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.37e-11
169.00
100.00%
97.06%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214.50
78.33%
78.33%
20.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-9
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                         JS-10-079-754A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-079-754A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                         265 TITCAACAATACCAGCCATAICAACGATATCCACTAAATTATCCTCCTGCGTATCCA
                                                                                                                                                                                                                       214 TCATCTGAAGAAACGTCACAGGAAACGGAAAAAACATCAT 255
                                                                                                                            21 SerSerGluGluLysArgHisArgLysArgLysLysHisHis 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000118
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-4 (1-604) x US-10-079-754A-11 (1-21)
                                   US-10-079-754A-4 (1-604) x US-10-079-754A-9 (1-70)
            Gaps:
                                                                                                                                                                          US-10-079-754A-11

Sequence 11, Application US/10079754A; Publication No. US2020164625A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 168, Application US/10210172
Publication No. US20040043928A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Petturajan, Merra
APPLICANT: Pena Carol
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Schusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112.00
100.00%
94.74%
10.88%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
```

```
154 AIGAAGAICITIAICITIGICITCAITAIGGCICICACCAAGCCAIGAITAGAGCIGAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| |||:::|||
| MetlysphepheValPheAlaLeulleLeuAlaLeuWetLeuSerMetThrGlyAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Benearly, Stephane
APPLICANT: Branka, Hiroaki
TILE OF INVENTION: Hiroaki
TILE OF INVENTION: HIROAKI
FILE REFERENCE: 91.034.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: PCT/IBOL/01715
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 TCATCTGAAGAGAAACGTCAC---AGGAAAACGGAAAAAAAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-4 (1-604) x US-09-917-340-19 (1-51)
                                                                                                             PAGENT NO. USCULLONS STATEMENT NO. USCULLONS STATEMENT NO. USCULLONS STATEMENT NO. USCULLONS STATEMENT NO. Christopher J. APPLICANT: McAnulty, Jonathan F. APPLICANT: Reid, Ted W. TITLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468 CURRENT APPLICATION NUMBER: US/09/917,340 CURRENT FILING DATE: 2001-07-28 PRIOR APPLICATION NUMBER: 60/290,932 PRIOR FILING DATE: 2000-01-17 PRIOR PLING DATE: 2001-05-15 PRIOR FILING DATE: 2001-05-15 NUMBER: OF SEQ ID NOS: 96 SUFWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AGAGGATATTTTCAACAATAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/0992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgGlyTyrArgSerAsnTyr 47
                                                            Sequence 19, Application US/09917340; Patent No. US20020090369A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.00
59.57%
46.81%
9.23%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-992-600A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-917-340-19
                                           -09-917-340-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Malyankar, Uriel
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TCATCTGAAGAGAAACGTCACAGGAAAACGAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SersergludlulyspheLeuargarglleGlyargPheGlyTyrdLyTyr---GlyPro 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/329,501
PRIOR FILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-08-09
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 TyrglnProValProGluGlnProLeu---TyrProGlnProTyr 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-4 (1-604) x US-10-210-172-168 (1-62)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.000307
110.00
61.82$
49.09$
                                                                                                                                                                                                                                            Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
                                                                                                                                                                                           Zhong, Mei
Gerlach, Valerie
                                                                                                                                    Anderson, David
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                            llerman, Karen
Voss, Edward
Boldog, Ferenc
Gorman, Linda
                                                                                                          Vernet, Corine
                                                                             Leite, Mario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-210-172-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                   APPLICANT
                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Пр
```

---CAT 255

51 6 13 6 2

S

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-999-570-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                             ò
                                                                    g
                                                                                                      \dot{\delta}
                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                        154 AIGAAGAICTITAICTITGICITICATIAIGGCICICAICCIAGCCAIGAITAGAGCIGAI 213
                                                                                                                                                                                                                                                                                                                                                                    214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                         Sequence 6. Application US/09924340

Publication No: US20030027248A1

Publication No: US20030027248A1

GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US2.REG
CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT APPLICATION NUMBER: US 60/305,456

PRIOR PLING DATE: 2001.08-06

PRIOR PLING DATE: 2001.07-13

PRIOR PLING DATE: 2001.06-13

PRIOR PLING DATE: 2001.06-15

PRIOR PLING DATE: 2001.06-15

PRIOR PLING DATE: 2001.06-15

PRIOR FILING DATE: 2001.06-15

SPIOR FILING DATE: 2001.06-15

SOFTWARE OF SEQ ID NOS: 112

SEQ ID NO 6

LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                               274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                                                                        |||| |||:::::: |||
21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: :::
---GluLysHisHisSerTyrHisIleThrLeuLeuProLeuPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
113
17
                                                                                                                                                                     7
113
7
7
                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                          US-10-079-754A-4 (1-604) x US-09-992-600A-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-079-754A-4 (1-604) x US-09-924-340-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                  94.50
56.36%
32.73%
9.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.50
56.36%
32.73%
9.18%
                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-09-992-600A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1..19
US-09-924-340-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-924-340-6
                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                   red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                    à
```

154 ATGAAGATCTTTATCTTTGTCTTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213

```
154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TCATCTGAAGAAACGTCACAGGAAACGGAAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                    214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||
| MetLysPhePheValPheAlaLeuValLeuAlaLeuMetIleSerMetIleSerAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WS-09-992-095B-6

Sequence 6, Application US/0992095B

Publication No. US20030157485A1

GENERAL INFORMATION:

APPLICANT: Benjainin, Stephane

APPLICANT : Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/992,095B

CURRENT FILING DATE: 2003-02-20

PRIOR PELING DATE: 2001-08-06

PRIOR PILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR PILING DATE: 2001-06-5

NUMBER OF SEQ ID NOS: 112

SSPCIDNOS:

SSPCIDNOS:

SSPCIDNOS:

SSPCIDNOS:

SSPCIDNOS:

SSECIDNOS:

SSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                   274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                 ::: | | | ::: | | | 35 ---GluLysHisHisSerTyrHisIleThrLeuLeuProLeuPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 SerHisGluLysArgHisHisGlyTyrArgArgLySPheHis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
113
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-4 (1-604) x US-09-992-095B-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09999570
Publication No. US20030170628A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.50
56.36%
32.73%
9.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-992-095B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
```

```
154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TCATCTGAAGAGAAACGTCACAGGAAAAAAAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091USOBDIV
CURRENT APPLICATION NUMBER: US 09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR PAPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: PCT/IBO1/01715
PRIOR PRIOR APPLICATION NUMBER: DCT/IBO1/01715
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Browning.
APPLICANT: Fanaka, Hiroaki
TILEOF ENVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.086.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT APPLICATION NUMBER: US/24,340
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GluLysHisHisSerTyrHisIleThrLeuLeuProLeuPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
18
13
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-079-754A-4 (1-604) x US-09-999-570-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10000489
Publication No. US20030092011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.50
56.36%
32.73%
9.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1..19
US-09-999-570-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-000-489-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

```
214 TCATCTGAAGAGAACGTCACAGGAAACGGAAAAAAACATCATAGAGGATATTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AIGAAGAICITIAICITIGICITICAITAIGGCICICAICCIAGCCAIGAITAGAGCIGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JULIOUOUSBEAND NO. USZ0030095247A1

GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
ITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.093.DIV
CURRENT APPLICANTON NUMBER: 10010/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/296,698
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/296,698
PRIOR PILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
18
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-4 (1-604) x US-10-000-489-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0238
94.50
56.36%
32.73%
9.18%
                                                                                                                                                                                                                                                                                               94.50
56.36%
32.73%
                                                                                                                                                                                                                                                                                                                                                           9.18%
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-10-000-986-6
                                                                                                                                                        NAME/KEY: SIGNAL LOCATION: 1..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-000-986-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: JPS
SEQ ID NO 6
LENGTH: 78
                                                                                                                                                                                                  US-10-000-489-6
                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

34

```
154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                  154 AIGAAGAICTITAICTITGICITCATTAIGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
                                                                                                                                                                      214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAAATTTTTCAACAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||
| MetLysPhePheValPheAlaLeuValLeuAlaLeuMetlleSerMetlleSerAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetLysPhePheValPheAlaLeuValLeuAlaLeuMetIleSerMetIleSerAlaAsp 20
                                                                                                                                                                                                                                                                                                                                                                MES-10-154-678-6

Sequence 6, Application US/10154678

Sequence 6, Application US/10154678

Publication No: US20030162186A1

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephane

APPLICANT: Benjamin, Stephane

APPLICANT: Tanaka, Hiroaki

TILE REFERENCE: 182.US1.REG

CURRENT APPLICATION: HUMAN CNNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 182.US1.REG

CURRENT APPLICATION NUMBER: US/10/154,678

CURRENT FILING DATE: 2001-01-5

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 6

LINGTH: 78
                                                                                                                                                                                                                                                             274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTAT 318
                                                                                                                                                                                                21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                       US-10-079-754A-4 (1-604) x US-10-000-986-6 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-079-754A-4 (1-604) x US-10-154-678-6 (1-78)
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 6, 2004, 17:24:49 Job time : 49.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.50
56.36%
32.73%
9.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-10-154-678-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                  ò
                                                                                                                                                                      à
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

This Page Blank (uspto)

```
August 14, 2004, 05:31:03 ; Search time 2769 Seconds (without alignments) 9454.385 Million cell updates/sec
                                                                                                                                                                                      1 gaagtattttcagttctata......tatcaagcataaaaaaaa 604
                                                                                                                                                                                                                                                                                                     6940544
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                      IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_htg_mam:
em_sy:*
em_sy:*
em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em htg hum: *
em htg_inv: *
em htg_other: *
em htg_mus: *
em htg_pln: *
em htg_rod: *
em htg_rod: *
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                       US-10-079-754A-4
604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95_htg:*
95_ov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_ba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             GenEmbl:*
                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                      Searched:
                                                                                              Run on:
                                                                                                                                                           Title:
```

Pred. No. is the number of results predicted by chance to have a

		æ			SUMMARIES	
sul No	Score	Query Match	Length	DB		Description
	141	23.3	95534	1	5	C134173 Bos tau
		ď	. 56	σ	BC017835	17835 Homo s
m	٢	ά.	23	6	AK131070	131070 Ното ва
4	'n	ď	in	9	BD071675	071675 Secrete
ហ	Ċ,	ä	m	9	AX588147	38147 Sequ
G	ċ	ä	m	9	AX588483	88483 Sequen
7	ċ	ä	m	φ	AX616321	16321 Sequen
œ	68.2	11.3	524	σ (HUMHISSX	Human 1 Hama
on (-i .	ט נ	א כ	BCOUG/VI	29/91 HOMO S
⊃ F	, a		νa	ט ת	AK120514	30503 Homo s
1 5			, L	νσ	AK130505	505 Homo 8
ا ا			4	σ	HIMSTTRNA	'1 Human st
14			വ	יסי	HUMSTATHA	78 Human st
15	7	Ή.	8	ø	AX747668	'668 Sequen
16	7.	Ή.	æ	σι	AK092678	678 Homo s
17	۲.	ä	0	9	BD071749	.749 Secret
18	ů,	i.	æ	σ	HUMHIS1X	4 Human his
19	'n.	°.	œ	4,	AY154893	1893 Bos tau
20	ď.	ö	O)	0	HUMBHRPA	'2 Human hi
21	ö	0.	\vdash	9	BD071674	674 Secrete
22	ö	ö	54	9	AX772840	840 Sequenc
23		o.	vo	7	AC094531	531 Rattus
24		ö	4044	7	AC131219	219 Rattus
c 25	0	·.	8459	0	0	950 Rattu
26	σ,		755	σ,	HUMHIS102	12 Human r
27	σ,		56	σ,	AC063956	200
28	o,		8596	~ (AC069037	103/ HOMO
0,	Ġ,		4384	7 (AC134934	1934 BOS L
30	٠ س		500	71 (AC1341/3	11/0
m) (٠		7 7 6 7	٠ م	BDO/L/SI	FOA DOCK
2 6	ι		0 0	٦ ,	DAZ46304	847 HOMO
ግ ‹	ິເ			۷ ۲	ACO1004	nos Dlacm
י ני	٩,		100	1 1	ABOLL 4020	SENE Diction
0 C	÷.		4 1	1 (ACEL 1000	200
י ריי	•		⊃ r	י ני	AE014834	ביר מסמי
0	4.		5407	n (AC115598	3330 Dictyon
י היו	4.		2000	7) (AE0148ZI	TOOL FLASHIOU
39	m i		1344	، م	AX346287	מפום יכפו
4,			200	η (AE014824	AAA PAABIIOO
4,			450	7) (7	A1392442	77.70
Ω 42	N		8213	n	ACII5684	0004 DICLYO
4,	52		8	'n	0048	1887 Zebrar
Ω 44	ഹ		4998	9	3445	1567 Seque
•			5443	r	2	CHUCA

AC134173

Bos taurus clone RP42-254113, WORKING DRAFT SEQUENCE, 26 unordered pieces.

NAC134173.
AC134173.
AC134173.
AC134173.1 GI:23306007

HTG; HTGS PHASE1; HTGS DRAFT.

Bos taurus (cow)
Sos taurus (cow)
Mammalia; Butheria; Craniata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos taurus (com)
Mammalia; Butheria; Catartiodactyla; Ruminantia; Pecora; Bovoidea; Marmy, D.M., Adams, C., Adio-Oducla, B., Ali-osman, F.R., Allen, C., ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AC134173/c LOCUS DEFINITION REFERENCE AUTHORS

ALIGNMENTS

```
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                   NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8311
8411
111103
111103
111103
111103
11143
11448
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
11418
1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95827
.05055
.05155
116717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150688
150788
166415
166515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
Alsbrocks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarda, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bonie, S., Birewa, M., Brown, B., Brown, B., Brown, C., Carron, T., Chen, G., Cher, G., Carter, M., Carces, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Doyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Doyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Terraguo, D., Flaggio, C., Elhaj, C., Escotto, M., Farnlart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Farlls, T., Ferraguo, D., Flaggio, V., Hale, S., Hamilton, K., Gabisia, A., Gaore, T., Hale, S., Hamilton, K., Harris, C., Harris, K., Hark, M., Halle, S., Hamilton, K., Harris, C., Harris, K., Hark, M., Holmson, Y., Ulloway, C., Hodison, A., Hogues, M., Holloway, C., Hodison, B., Jia, Y., Johnson, R., Joliver, S., Joudah, S., Karlsson, E., Kalls, T., Johnson, R., Joliver, Korah, J., Kovar, C., Karlson, E., Kalls, M., Lindary, W., Leal, B., Lewis, L., Louiseged, H., Loado, M., Manuer, G., Miner, G., Martin, R., Martindale, M., Malou, P., Martin, R., Martindale, M., Malou, P., Morden, M., Massey, E., Mawhiney, E., Malliney, E., Mallin, M., Mapuu, P., Martin, R., Martindale, M., Malou, P., Morden, M., Okwnon, G., Ordun, M., Okwnon, G., Ordun, M., Okwnon, G., Ordun, M., Okwnon, G., Scherer, B., Nachen, R., Nachen, M., Sisson, I., Ruse, S., Rolubokan, T., Rolfe, M., Naloson, M., Ward, Morgen, M., Vinson, R., Mard, Morder, S., Scott, G., Shen, H., Shooshtari, N., Mard, Morce, S., Marren, R., Washington, C., Wang, S., Walliamson, A., Willers, M., Walliams, S., March, M., Stor, H., Mard, S., Walliams, S., March, M., Shooshtari, N., Walliams, S., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (24-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 195534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-58P-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: VUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 [bases 1 to 195534)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
```

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

as contig of 2358 bp in length contig of 3161 bp in length contig of 3161 bp in length contig of 3161 bp in length contig of 2591 bp in length contig of 2592 bp in length gap of unknown length contig of 2832 bp in length contig of 2848 bp in length contig of 2863 bp in length contig of 2863 bp in length gap of unknown length contig of 3657 bp in length contig of 3857 bp in length contig of 3857 bp in length contig of 5837 bp in length contig of 6038 bp in length gap of unknown length contig of 6038 bp in length contig of 6038 bp in length gap of unknown length contig of 6038 bp in length contig of 6038 bp in length contig of 6038 bp in length

25171: 25271: 21514:

30645:

41956: 48094: 53214: 58849: 58949: 66144: 73033:

5719:

11002: 14486: 17249:

```
ö
                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                       23.3%; Score 141; DB 2; Length 195534; 100.0%; Pred. No. 2.3e-17; cive 0; Mismatches 0; Indels 0;
gap of unknown length contig of 29020 hr '-'
                                                                                                          /mol_type="genomic DNA"
/db xref="taxon:9913"
                                                                                           /organism="Bos taurus"
                                                                                                                                        /clone="RP42-254I13"
                                                            Location/Qualifiers
                                                                                                                                                                                           Query Match 23.3
Best Local Similarity 100.
Matches 141; Conservative
                                                                                                                                                                                                                                                            δ
```

3: contig of 11477 bp in length 3: gap of unknown length 0: contig of 9747 bp in length 0: gap of unknown length 7: contig of 12447 bp in length 7: gap of unknown length

unknown length of 15627 bp in

150687: 166414: 166514:

contig of 11562 bp in length

unknown length

gap of

116816: 128393:

igap of unknown length contrig of 6789 bp in length contrig of 6789 bp in length contrig of 6897 bp in length gap of unknown length contrig of 7813 bp in length contrig of 7865 bp in length contrig of 7865 bp in length gap of unknown length contrig of 9228 bp in length gap of unknown length gap of unknown length gap of unknown length

87861:

gap of unknown length contig of 5020 bp in length gap of unknown length contig of 5535 bp in length gap of unknown length contig of 7195 bp in length

66244:

ð g Š

```
/codon_start=1
/product="histatin 1"
/protein_id="AAH17835.1"
/db_xref="1G1:1739615.1"
/db_xref="LocusID:3346"
/db_xref="LocusID:3346"
/db_xref="NocusID:3346"
/db_xref="NocusID:3346"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 10-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GAATTICATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAAACATCATGGGTA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y.; Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAAGGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2008 ggacraricaaarrarcrarargacaarrgararccriragrarcargggggargar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 cacrerererisagraaaagacreagecaacrargaagrirrirgecriragr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 77; DB 9; Length 566
Similarity 59.8%; Pred. No. 7.3e-05;
50; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3235 bp mRNA line
Homo sapiens cDNA FLJ29036 fis, clone SLV00594.
AK131070.
AK131070.1 GI:34528324
                                                                             /mol_type="mRNA"
/db_xref="teaxon:9606"
/db_xref="teaxon:9606"
/clone="MGC:22502 IMAGE:4289874"
/tissue_type="Skeletal Muscle"
/clone_lab="NIH MGC_81"
/lab_host="DH108"
/note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo capping, fis (full insert sequence)
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugano, S.
NEDO human cDNA sequencing project
Unpublished
                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                  /note="synonym: HIS1"
/db_xref="LocusID:3346"
/db_xref="MIM:142701"
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 3235)
Sugano, S. and Suzuki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYGDYGSNYLYDN"
                                                                                                                                                                                                                                                                                              gene="HTN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 TATAGAGGITT 278
                                                                                                                                                                                                                                                                       . . 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
AK131070
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                             CDS
     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 566)
Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K. Bamado, M.F., Casavant, T.L., Stepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheeter, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gararatne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Marny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Banty, D.M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Mann, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Zonos, S.J. and Marra, M.A.
  WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rømall.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL plate: 3 Row: a Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21359863.
                                                                                                                                                                                                                                                                                                                                                                                 p mRNA linear PRI 04-OCT-2003 (cDNA clone MGC:22502 IMAGE:4289874),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web Site: http://www-sngc.stanioiu.cuu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R.
Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                     GGATTICAAGGIAITIAAACACAGCAGITITICIAGCAAAGAACAICICCIGAAGCAICAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                 BC017835 56 bp
Homo sapiens histatin 1, mRNA (c
complete ods.
                                                                                                                                                                                                                                                47245 AATTTCATCTTCATGACTGG 47225
                                                                                                                                                                                               121 AATTICATCTITCATGACTGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC017835
BC017835.1 GI:17389614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12477932
                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                RESULT 2
BC017835
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

ï

267

us-10-079-754a-4.rge

```
Topology: Linear;
Secreted expressed sequence tags (SESTs)
                                                                                                                                                                                                                                         Score 75.4; DB 6;
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84. ... 320
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /proteIn id="CAD61372.1"
/db_xref="GI:27899823"
/db_xref="REMTREMBL:CAD61372"
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 from Patent W002083898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                               1. .357
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX588147.1 GI:27899822
                                                                                                                                                                                                                                       12.5%;
nilarity 59.4%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397. .402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATAGAGGTTT 292
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                            source
Double;
CC Top
CC Sec
FH Key
FT sou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_signal
polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                Matches 149;
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                Local
                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
AX588147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                            ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                          Fax:81.3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΒI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2730 GACTCTCCTCTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT 2789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ragaagaaaarrccar----gaaaagcarcarrcacarcgagaarrrccarrrargg 2903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2904 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 2963
 Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F 10-APR-1998 JP 1998543069
F 10-APR-1997 US 08/838821
I KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, DAVID MERBERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2790 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 357)
Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino.M.J.
Secreted expressed sequence tags (sESTs)
Batent: JP 2001:19667-A 485 23-OCT-2001;
GENETICS INSTITUTE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 77; DB 9; Length 323
Pred. No. 5.5e-05;
0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                       /tissue type="salivary gland"
/clone_lib="SLV"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted expressed sequence tags (sESTs).
BD071675.1 GI:22617278
JP 200151946.7 2.2617278
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SLV00594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
JP 2001519667-A/485
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.8%;
Matches 150; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2964 raradadgrir 2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
BD071675
LOCUS
                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

ઠ 셤 ઠે g δ d ઠ્ઠે g

ò

```
/translation="wkefvpalvlalmismisadshekrhhgyrrkfhekhhsyhitl
Lplfeessksnanekhynllytlcfrilafsivt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GAATTICATCTITICATGACTICCACCACCAAATATGAAGATCTITATCTITGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 ACGGAAAAACATCATAGAGGATATTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 TAGAAGAAATTCCAT-----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 ggacricrogarcaarrarcrarargacaarrgararccrragraarcargggggrafigar 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bejanin,S., Tanaka,H., Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
Full-length human cdnas encoding potentially secreted proteins
Patent: WO 02083898-A 22 24-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84. .140
/note="Von Heijne matrix score 7.64030745849671 seq
ALVLALMISMISA/DS"
                                                                                                                                                                                                                                                                                                                                                                                      .
9
                                                                                                                                                                                                                                                                                                                           Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                      96; Indels
Location/Qualifiers
1. .357
/organism='Unidentified'
```

```
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
PUBMED
                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
HUMHIS2X
                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product"
/codon start=1
/protein id="CAD61539.1"
/brotein id="C127900157"
/db xxfef="REMTEMBL: CAD61539"
/translation="MKPFVFALVIALMISMISADSHEKRHHGYRRKFHEKHHSYHITLIPLESSKSNANBKHYNLLYTLCFRILAFSIVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                PAT 24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GAATTICAICITICAIGACTGGACTCCAACAATATGAAGATCTTTAICITIGICTTCAI 179
                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bejanin, S., Tanaka, H., Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
Full-length human cdnas encoding potentially secreted proteins
Patent: WO 02083898-A 358 24-OCT-2002;
GENSET (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                   180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTOTOCTOTTGAGAGACTCAGCCAACTATGAAGTTTTTTGTCTTTTGCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84. .140
A/Unctal-Von Heijne matrix score 7.5999990463257
A/Uncal-WarSMISA/DS"
                                                               ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.7%; Score 70.4; DB 6; Length 438; Best Local Similarity 69.9%; Pred. No. 0.0013; Matches 95; Conservative 0; Mismatches 41; Indels
                              Length 438;
                          Query Match
11.7%; Score 70.4; DB 6; Length 4
Best Local Similarity 69.9%; Pred. No. 0.0013;
Matches 95; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                      AX588483 438 bp DNA
Sequence 358 from Patent WO02083898.
AX588483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
84. .320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                AX588483.1 GI:27900156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                 170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                 240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                RESULT 6
AX588483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \dot{\delta}
                                                                                                                                                                                                                                 ò
```

RESULT 7 AX616321

```
64. 320

/note="unnamed protein product"

/notein_id="CAD67625.1"

/protein_id="CAD67625.1"

/db_xref="E1:28447366"

/db_xref="REMTREMBL:CAD67625"

/translation="WRFFVFALVLALMISMISADSHEKRHHGYRRKFHEKHHSYHITL
IPLFBESSKSNANEKHYNLLYTLCFRILAFSIVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 31-DEC-1994
               PAT 20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GAATTICATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         so cacrcrcrrcagrada accacrca con cantal de la cacreta de l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 ctidectotoateatricoateatracecteatroacateaaaaaacacateatea 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 524)
Sabatini,L.M. and Azen,E.A.
Histatins, a family of salivary histidine-rich proteins, are encoded by at least two loci (HIS1 and HIS2)
Biochem. Biophys. Res. Commun. 160 (2), 495-502 (1989)
                                                                                                                                                                                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source text: Homo sapiens parotid gland cDNA to mENA.
Location/Qualifiers
1. .524
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.7%; Score 70.4; DB 6; Length 438; Best Local Similarity 69.9%; Pred. No. 0.0013; Matches 95; Conservative 0; Mismatches 41; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMHIS2X 524 bp mRNA
Human histatin 2 (HIS2) mRNA, complete cds.
M26665.
M26665.1 GI:292145
M1statin 2.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bejanin,S. and Tanaka,H.
Human cdinas and proceins and uses thereof
Patent: WO 02094864-A 5 28-NOV-2002;
GENSET (FR)
                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1 .83
Sequence 5 from Patent WO02094864.
                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                               AX616321.1 GI:28447365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ACGGAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
polyA_site
ORIGIN
```

be found

```
/product="histatin 3"
/protein_id="AAH09791.1"
/db_xref="GI:14602561"
/db_xref="LocusID:3347"
/translation="MKFFVFALILALMLSWTGADSHAKRHHGYKRKFHEKHHSHRGYR
SNYLYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 10-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 CTTGGCTCTCATGCTTTCCATGACTGGAGCTCATTCACATGCAAGAGACATCATGGTA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557652.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mark Ketteman, Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTTCAT
                                                                                                                                                                                                                                                                                                                                                              http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Anadan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                           Consequence of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.3%; Score 68.2; DB 9; Length 5
Best Local Similarity 65.4%; Pred. No. 0.0034;
Matches 100; Conservative 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1824 bp mRNA linear
Homo sapiens cDNA FLJ26103 fis, clone SLV07780.
AK129614
                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonyms: HIS2, HTN2, HTN5"
/db_xref="LocusID:3347"
/db_xref="MIM:142702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="m2NA"
/mol_trpe="m2NA"
/clone="MGC:13578 IMAGE:4293405"
/clone="MGC:13578 IMAGE:4293405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 ACGGAAAAACATCATAGAGGATATTTCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 TAAAAGAAATTCCATGAAAAGCATCATTCACA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue type="Skeletal Muscle"
/clone lib="NIH MGC_81"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK129614.1 GI:34526191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="HTN3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
AK129614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                      REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Maax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavanch, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC009791 558 bp mRNA linear PRI 12-NOV-2003
Homo sapiens histatin 3, mRNA (cDNA clone MGC:13578 IMAGE:4293405),
complete cds.
                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MKFFVFALILALMLSMTGADSHAKRHHGYKRKFHEKHHSHRGYR
SNYLYDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GAATTICATCITICATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 criggcicicargcirrccargacrggagcrgarrcacargcaaagagacargagaa 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 GATTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTTTTTGCTTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68.2; DB 9; Length 5:
Pred. No. 0.0034;
0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ACGGAAAAACATCATAGAGGATATTTTCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 TAAAAGAAATTCCATGAAAAGCATCATTCACA 190
                   /db_xref="taxon:9606"
/tissue_type="parotid gland"
                                                                                                                                                                                                                                                                                                 protein_id="AAA58646.1"
/db_xref="GI:292146"
                                                                                                                                                                                                                                    /codon_start=1
/product="histatin_2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC009791.1 GI:14602560
                                                                                                                         gene="HIS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HIS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.4%;
Matches 100; Conservative
                                                                                                                                                                                              gene="HIS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 558)
                                                                                                                                                                   . 227
                                                                                           .524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC009791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
```

g

ઠ

d ò

ò

ö

Gaps

179

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

```
Sugano, S. and Suzuki, Y.

Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, Submitted (31-JUL-2003) Sumio Sugano, Structure, Human Genome Structure; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flocha@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5286, NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA FLJ26995 fis, clone SLV04017, highly similar to AK130505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2073 CTIGGCICTCAIGCTTICCAIGACTGAACTCATTCACAIGCAAAGAGACACATCAIGGGTA 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Suzuki, Y., Haete, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Izie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, T., Kawakami, B., Nagai, K., Isogai, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GAATITCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2013 GATTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTTTTTGCTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 2499 / Organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="texon:9606"
/clone="SIV03847"
/clone lib="SLV"
/note="Cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 68.2; DB 9;
Similarity 65.4%; Pred. No. 0.0027;
00; Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK130505.1 GI:34527322
oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2133 TAAAAGAAATTCCATGAAAAGCATCATTCACA 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 ACGGAAAAAAACAICAIAGAGGAIAITITCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugano, S.
NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 2537)
Sugano, S. and Suzuki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
AK130505
         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                    Direct Submission

Sugano, S. and Suzuki, Y.

Direct Submission

List Cabes 1 to 1824)

Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (J1-UUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of Fax:81-3-5449-5416

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Dapan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Home sapiens cDNA FLJ26993 fis, clone SLV03847, highly similar to Histatin 3 precursor.
AK130503.
AK130503.1 GI:34527320
oligo capping; fis (full insert sequence).
Home sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTTCATCTTTCATGACTGCACCACCAAATATGAAGATCTTTATCTTTGTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Skaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Mortinaga, M., Kawamura, M., Sugiyama, T., Itle, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
                         I.
Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,
Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1338 GATTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTTTTGCTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%; Score 68.2; DB 9; Length 1824; larity 65.4%; Pred. No. 0.0028; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1458 TAAAAGAAATTCCATGAAAAGCATCATTCACA 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 1824
Acadamse="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SLVV7780"
/tissue_type="salivary gland"
/clone_lib="sLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ACGGAAAAACATCATAGAGGATATTTTCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugano,S.
NEDO human cDNA sequencing project
Unpublished
                                                                                                                                                                                                                                   NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 100; Conserv
                                                                                                                                                                                                                                                                   Unpublished
```

Query Match

ORIGIN

FEATURES

Best Loca Matches

d à q ò LOCUS

RESULT 11 AK130503

d

ORGANISM

VERSION KEYWORDS SOURCE ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL

0

Gaps .,

Length 2499;

179

ω

2,

```
/protein_id="AAA60594.1"
/db_xref="G1:338508"
/db_xref="GD8:600-120-391"
/translation="MKELVPAFILALMVSMIGADSSEEKFIRRIGRFGYGYGPYQPVP
FQPLYPQPYQPQYQQYTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 13-JAN-1995
                                                                                                                                                                                                                                                                        140 GGACTCCACCAAATAIGAAGAICTITAICIITGTCTITCAITAIGGCTCTCTCATCCTAGCCA 199
                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable sequence [1] kindly submitted by L.Sabatini 19-JAN-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATGGCTCTCATGGTTTCCA 102
                                                                                                                                                                                                                                                                                                                                                     260 GATA-----TITITCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 gerangecectrarcagecagnecagaacaacaachanacaacaaacaraacaaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 552)
Sabatini,L.M., Carlock,L.R., Johnson,G.W. and Azen,E.A.
CoDA cloning and chromosomal localization (4q11-13) of a gene for statherin, a regulator of calcium in saliva
Am. J. Hum. Genet. 41 (6), 1048-1060 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Human parotid gland, cDNA to mENA, clone H772B.
Draft entry and computer-readable secuence [1] kindly submitted
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              6
                                                                                                                                                                                   Length 542;
                                                                                                                                                                                   Score 67.6; DB 9; Length 5 Pred. No. 0.0044; 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="STATH"
  /note="statherin signal peptide"
upstream of PstI site; chromosome 4q11-q13.
                                                                                                                                           262 bp upstream of PstI site; chromosome 4q11-q13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                        57. .113
/gene="STATH"
/note="statherin signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human statherin mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="statherin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/map="4q11-q13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory protein; statherin.
Homo sapiens (human)
                                                                                                                            product="statherin"
EQPLYPQPYQPQYQQYTF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                      /gene="STATH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="STATH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="STATH"
                                                                                                                                                                                     Query Match
Best Local Similarity 61.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M18078.1 GI:338507
                                                                              .242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73. .261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMSTATHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88074310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M18078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 bp
                          sig_peptide
                                                                                       mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
HUMSTATHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
Economy, Trade and Industry of Japan, cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.

1. .2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57. ..245

Gene="GTATH"

/note="start=1

/protein_id="AAA60600.1"

/bx xref="GI:338611"

/db_xref="GGB:300-120-391"

/tb_xref="GGB:300-120-391"

/tb_xref="GGB:300-120-391"
                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickinson, D.P., Zidall, A.L. and Levine, M.J.
Human submandibular gland statherin and basic histidine-rich
peptide are encoded by highly abundant mRNA's derived from a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2051 GATTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTTTTTGCTTTAAT 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 CTTGGCTCTCATGCTTTCCATGACTGGACTGATTCACATGCAAAGAGACATCATGGGTA 2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 13-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 542)
Dickinson, D. P., Ridall, A.L. and Levine, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTICATCTTTCATGACTGGACTCCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Human female submandibuar gland, cDNA to mRNA, clone pBRHSWSF9B8.2.

Draft entry and computer readable copy of sequence [1] kindly provided by D.P.Dickinson 21-MAR-1988.

1. .542
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                           Length 2537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 149 (2), 784-790 (1987)
88106506
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                /tissue type="salivary gland"
/clone_lib="SLV"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 68.2; DB 9; 65.4%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2171 TAAAAGAAATTCCATGAAAGCATCATTCACA 2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAAACATCATAGAGGATATTTTCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMSTTRNA
Human statherin mRNA, complete cds.
                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SLV04017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="4q11-q13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STATH"
57. .245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M18371.1 GI:338610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seguence
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        statherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3426601
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
HUMSTTRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
```

d ð g à g

```
linear PAT 20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083 gaacccagccaacrargaagrrccrrgrcrrrgccrrcarcrrgscrcrcargerrcca 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143 TGATTGGAGCTGATTCATCTGAAGAGAAATTTTTGCGTAGAATTGGAAGATTCGGTTATG 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1263 AATACCAACAATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 1322
                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 GATA-----TITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 CGT---AICCAITICCTIAAAAIGCTGCTIAGIAACTACAGGACAIGAITAGAGAGAIII 370
                                                                                         199
                                                                                                                                                                                                       59 GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATCTTGGCTCTCATGGTTTCCA 118
                                                                                                                                                                           260 GATA-----TITICAACAATACCCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                          314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                 239 AATACCAACATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCTAGCCA
                                                                                         140 GGACTCCAACAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length cDNA sequences
Full-length cDNA sequences
Patent: EP 1308459-A 1193 07-VAY-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
Location/Qualifiers
                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.2%; Score 67.6; DB 6; Length 1584;
Best Local Similarity 61.2%; Pred. No. 0.0037;
Matches 147; Conservative 0; Mismatches 84; Indels 9;
Query Match 11.2%; Score 67.6; DB 9; Length 552; Best Local Similarity 61.2%; Pred. No. 0.0044; Matches 147; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX747668 1584 bp mRNA Sequence 1193 from Patent EP1308459. AX747668 1 GI:32132056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1584
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 15, 2004, 22:31:24 Job time : 2774 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masuho, Y.
                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AX747668
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                            셤
                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                      a
```

Ipis bade Blank (nsbto)

```
August 14, 2004, 05:08:11; Search time 352 Seconds (without alignments) 7289.522 Million cell updates/sec
                                                                                                                                                                                                                         1 gaagtattttcagttctata.......tatcaagcataaaaaaaaa 604
                                                                                                                                                                                                                                                                                                                                                     6747726
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:*
geneseqn2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_29Jan04:*
1: geneseqn1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqn2001as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqn2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geneseqn2003cs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genesegn1980s:*
genesegn1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqn2000s:*
                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                               US-10-079-754A-4
604
                 Copyright
                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                            Scoring table:
                                                                         OM nucleic
                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abx11391 Bovine hi	Abx11388 Bovine hi	Abx11389 Bovine hi	Abx11393 Bovine hi	Abx11394 Bovine ma	Abx11390 Bovine hi		Aav89526 EST clone	Acc51062 Human Chi	Abz36590 Human GEN	Abz36425 Human GEN	Aah98658 Human EST	Aaa48964 Human sta	Ade40261 Human NOV	Adb63039 Human cDN	Aav89600 EST clone	Aaa48965 Human bas		VON 6	Aav89525 EST clone	Aal60905 Human sal	00	Abq99552 Human cod
	ID	ABX11391	ABX11388	ABX11389	ABX11393	ABX11394	ABX11390	ABX11392	AAV89526	ACC51062	ABZ36590	ABZ36425	AAH98658	AAA48964	ADE40261	ADB63039	AAV89600	AAA48965	ADE09636	ADE07409	AAV89525	AAL60905	AAL61238	ABQ99552
	DB	7	7	7	۲	7	7	7	~	7	7	7	4	m	σ	on	N	m	σ	σ	~	α	ထ	9
,	° Query Match Length DB	604	505	585	525	267		96	357		438	438	857	552	678	1584	203	491	406	417	516	548	732	457
d	Query Match	100.0	77.1	74.2	70.1	39.5	19.0	14.4	12.5	11.7	11.7	11.7	11.3	11.2	11.2	11.2	11.1	10.4	10.3	10.1	10.1	10.1	9.9	9.6
	Score	604	465.4	448.2	423.4	238.4	115	87	75.4	70.4	70.4	70.4	68.2	67.6		67.6	67.2	62.6	62	60.8	60.8	60.8	59.6	58
	Result No.		7	ო	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18			21		23

24	ம		176	0	960	9602 EST cl	
7	53.6		13449	9	ABL33385	385	_
C	\vdash		6255	φ	ABL32961	296	_
l (V			12507	φ	ABL32298	2298	_
100	51		257	4	AAS46659	in	
29	49.8	8	7106	9	347	œ	_
m	ത		5945	9	ABL32084	984	_
. (**	o		669	9	ABL32989	989	_
m	49.2		13131	9	ABL92249	48	
m	49		2000	٢	ADA71938	38	
m	49		33	9	ABL34125		_
m	49		73334	9	ABL92319	13	
m	47.8		78	9	ABL32777	111	_
m	-		6274	4	AAS46321	1 Tumon	_
m	r		6274	9	ABK31238	œ	
m	47.6		6274	7	ADA20354	4	
4	47.6		6274	7	ADA84161	61	_
4	7		6274	σ	ADB54121	N	٠.
4	~		6274	σ	ADB54249	9	
4	7		19659	φ	ABL32766	Abl32766 Human imm	_
4	7		615	φ	m	28362 DNA tran	
c 45	۲.	•	6280	φ	ABL92265	Ab192265 Chemicall	
					ALIGNMENTS		
RESULT 1 ABX11391						•	

```
New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                                         Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial.
                                                                                                                                                                                                                          /*tag= a
/product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                             Molenaar AJ, Davis SR;
                                                                       Bovine histatin like polypeptide, #4, cDNA.
                                                                                                                                                                                                Location/Qualifiers
154. .330
                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
琚.
                                                                                                                                                                                                                                                                                                                                     23-AUG-1999; 99US-0150330P.
29-OCT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                                                                 19-FEB-2002; 2002US-00079754.
ABX11391 standard; cDNA; 604
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-275306/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG75794.
                                                                                                                                                                                                                                                                US2002164625-A1.
                                                 01-MAY-2003
                                                                                                                                                                                                                                                                                        07-NOV-2002.
                                                                                                                                                                           Bos taurus
                       ABX11391;
                                                                                                                                                                                                   Key
```

ABX11388 standard; cDNA; 505

(first entry)

01-MAY-2003

ABX11388;

Claim 1; Page 12; 17pp; English

 $\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{X}}\overset{\circ}{\mathbf{A}}\overset{\circ}$

```
RESULT 2
               ABX11388
                                 conjugated by which computes sequences expressed in bovine. Histatins are histidine rich and specific to the salivary secretions. They are believed to the function as part of the non-immume defence system, particularly in the cardical cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral candidesis. Also disclosed are compositions comprising the histatin polymucleotide, and at least one component consisting of polypeptide or polymucleotide, and at least one component consisting of histatin polymucleotide, and at least one composition or polypeptide, polypeptide, or the cosmetic composition or instatin polymucleotide is useful for treating (e.g. gene therapy) a discrete in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful in genome mapping, physical mapping or in the positional cloning of genes. Specifically, the colypeptide or polymucleotide is useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by Pseudomonas aerudinosal, mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or polymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine treating mastitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATTTCAAGGTATTTAAACACAGCAGTTTTCTAGCAAAGAACATCTCCTGAAGCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGCTCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGAAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGTTGAAAACCATCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITCITITICICIGICACTIACCAIGCAIGCTIAATAAATIGAICTAICAAGCAIAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITCITITICITICACTIACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGAGATITITICACAATGATITITICCTACTCTITICIGITGTTGAAAACCATCTITICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGAATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                     Length 604;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 604 BP; 222 A; 112 C; 79 G; 191 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 604; DB 7; L 100.0%; Pred. No. 5.2e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
 invention discloses isolated histatin
                                                                                                                                                                                                                                                                                                                                                                                                                                       604; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

dd

ઠ В g 8 g ò ad ð

ð

g

ઠે g ò g

```
The invention discloses isolated histatin polynucleotides and polypeptides, which comprise sequences expressed in bovine. Histatins are historine rich and specific to the salivary secretions. They are believed to finite find the specific to the salivary secretions. They are believed to complete as part of the non-immune defence system, particularly in the cardidosis. Also disclosed are compositions comprising the histatin composition or polypeptide or polymucleotide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The histatin polymucleotide, polypeptide or the comment omposition of comprising the polypeptide, is useful for treating (e.g. gene therapy) a disorder in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful for treating (e.g. gene therapy) a classification or in the positional cloning of genes Specifically, the polypeptide or polymucleotide is useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartari, caused by Pseudomonas aeroginas, mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or prolymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine treating mastitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                              Cow, gene, ss, histatin, bovine, salivary secretion, oral cavity, non-immune defence system, oral candidosis, gene therapy, microbial infection, fungal infection, dental caries, plaque; tartar; cystic fibrosis, systemic infection, Candida infection, mastitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SR.
Bovine histatin like polypeptide, #1, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
44. .220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molenaar AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1, Page 11; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1999; 99US-0150330P.
29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-0069146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-2002; 2002US-00079754
                                                                                                                                                                                                                                                                   fungicide; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 2003-275306/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABG75791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002164625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systemic
```

Sequence 505 BP; 188 A; 96 C; 67 G; 154 T; 0 U; 0 Other;

AAAA 604

601

g à d ð

ò

```
δ
                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                  임
                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                   \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                       ò
                                                                                                                                    377
                                       197
                                                                      257
                                                                                      147
                                                                                                                      207
                                                                                                                                                      267
                                                                                                                                                                     437
                                                                                                                                                                                     327
                                                                                                                                                                                                      497
                                                                                                                                                                                                                     387
                                                                                                                                                                                                                                      557
                                                                                                                                                                                                                                                     447
                                                     87
                                                                      88 cargarragagcrgarrcarcrgaagagaaacgrcacaggaaacggaaaaaaacarcarag
                                                                                                                     148 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                      TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA
                                                                                                                                                      208 rccarrrccrraaaargcrgcrracraacracaggacargarragagagarrrrrcacaa
                                                                                                                                                                     TGATTTTTCCTACTCTTTCTGTTGTTTGAAAACCATCTTTCAAATGAATAAAACAAAGA
                                                                                                                                                                                 328 AAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATCAATATTTAA
                                                                                                                                                                                                                                      Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis;
                                       138 CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCAGC
                                                 AGGATATTTTCAACAATACCAGCCATATCAAGGATATCCACTAAATTATCCTCCTGCGTA
                       Gaps
                       ..
        Length 505;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Histatin like polypeptide"
        7;
       Score 465.4; DB 7
Pred. No. 2.4e-90;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                             Bovine histatin like polypeptide, #2, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-1999; 99US-0150330P.
29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-0069146.
                                                                                                                                                                                                                                                                                                                              ABX11389 standard; cDNA; 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-2002; 2002US-00079754
        77.1%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .325
      Query Match
Best Local Similarity 99.8
Matches 466; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            fungicide; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002164625-A1
                                                                                                                                                                                                                                                                                                                                                              01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                       28
                                                                      198
                                                                                                       258
                                                                                                                                       318
                                                                                                                                                                      378
                                                                                                                                                                                                       438
                                                                                                                                                                                                                                       498
                                                                                                                                                                                                                                                                                      448
                                                                                                                                                                                       268
                                                                                                                                                                                                                                                                                                                                               ABX11389;
                                                                                                                                                                                                                                                                                                              Key
                                                                                      g
                                                                                                                    g
                                                                                                                                                      g
                                                                                                                                                                      à
                                                                                                                                                                                     В
                                                                                                                                                                                                      ð
                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                       ò
                                                                      ò
                                                                                                       ò
                                                                                                                                       ò
```

```
the invention unscuoses isometed install publications and installing and installing and installing confirms and specific to the salivary secretions. They are believed histidine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the coral cavity and have promise as therapeutic agents in humans with oral cardidosis. Also disclosed are compositions comprising the histatin of confidence or polymentoleotide, and at least one component consisting of physicological or plarmaceutical carriers or immunostimulants. The histatin polymucleotide, polypeptide, or the cosmetic composition of comprising the polypeptide, is useful for treating (e.g. gene therapy) a discret in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful in genome mapping, physical conspiculation or in the positional cloning of genes. Specifically, the comprision of the oral cavity (e.g. dental caries, plaque or tartar), or infections of the oral cavity (e.g. dental caries, plaque or tartar), or caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or polymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine constitution is the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552
                                                                                                                                            New histatin polymucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAAACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 rccarrrccrraaaargcrgcrragraacracaggacargarragagagarrrrrcacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATTTTTCCTACTCTTTCTGTTGTAAAACCATCTTTCAAATGAATAAAACAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAAATCAGTCAAGTTGCACAACACATTAGGAATCAAATATCAATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 caggacrocaccaaarargaagarcrrrarcrrrarcrrrargacrorcarccrage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AGGATATTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 rgartrirccracrerricrererereraaaaccarerreaargaaraaacaaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                               The invention discloses isolated histatin polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 585 BP; 215 A; 111 C; 85 G; 174 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.2%; Score 448.2; DB 7
99.3%; Pred. No. 1.2e-86;
live 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIACCATGCATGCTTAATAAATTGATCTATCAA 590
Davis SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rraccardcardcrraaraaarrdarcrarcaa
   Molenaar AJ,
                                                                                                                                                                                                                                                                                                               Claim 1; Page 11; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.3
Matches 450; Conservative
   Grigor MR,
                                                                                                                                                                                                                                                systemic infections
                                                               2003-275306/27
                                                                                          P-PSDB; ABG75792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
   Glenn M,
```

Length 525;

RESULT

```
US2002164625-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus.
                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX11394;
                                                                                               138
                                                                                                                                                                                                 198
                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                                                                                                                  286
                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
Query Match
Best Local $
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX11394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                            임
                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses isolated histatin polymucleotides and polypeptides, which comprise sequences expressed in bovine. Histatins are historial at the and specific to the salivary secretions. They are believed to chistidine rich and specific to the salivary secretions. They are believed to complete as part of the non-immune defence system, particularly in the cardidosis. Also disclosed are compositions compressing the histatin polypeptide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The comprising the polypeptide, for the cosmetic composition of histatin polypeptide, is useful for treating (e.g. gene therapy) a disorder in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful for treating fungal or bacterial histatin polymucleotide is also useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartarl, subjuncteotide is also useful for treating fungal or tartarl, or subjunctory tract (e.g. cystic fibrosis caused by pseudomonas aeruginosis), mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or polypuctide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine the histatin like polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                                                                                                                                                                                                                        Cow, gene, ss, histatin, bovine, salivary secretion, oral cavity, non-immune defence system, oral candidosis, gene therapy, microbial infection, fungal infection, dental caries, plaque, tartar, cystic fibrosis, systemic infection, Candida infection, mastitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis SR;
                                                                                                                                                                                                                              Bovine histatin like polypeptide, #6, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molenaar AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 13; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0162701P.
2000US-00644190.
                                                                               ABX11393 standard; cDNA; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-2002; 2002US-00079754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0150330P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00699146
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  fungicide; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-275306/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABG75796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002164625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1999;
29-OCT-1999;
22-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000;
                                                                                                                                                                            01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glenn M,
                                                                                                                               ABX11393;
                                                       ABX11393
```

C; 72 G; 164 T; 0 U; 0 Other;

Sequence 525 BP; 187 A; 102

```
326
                                                                                                                                                                                                                                                                                                                                                                                                                                                        386
                                                                                  197
                                                                                                                                                                                                                    285
                                                                                                                                                                                                                                                                                       345
                                                                                                                                                                                                                                                                                                                                                        405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Graatregrincratricritricricricactraccarecarecriaaraaraaricarer 506
                                                                                                                                                    255
                                                                                                                                                                                    146
                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAACCATCTTTCAAATGAATAAAAAAAAAAAAAAAATCAGTCAAGTAGTTGCACAA 465
                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cow; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial; mammary-gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAAACATCAT--
                                                                                                                                                                                                                                                                                      CAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAA
                                                                                                                                                                                                                                                                                                                      CACATACTTGGAATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTAATTGGTTTCTACTTTCTTTTCTCTGTCACTTACCATGCTTAATAATTGATCT
                                                                                                                   27 cassacriccaccaararsaasarcrirarcrirsrcrircarrarsscricarcricars
                                                                                                                                                                                     CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAACATGT
                                                                                                                                                                                                                      -----AGAGGATATTTTCAACAATACCAGCCATAT
                                                                                                                                                                                                                                                    TGATAGGTCTCCAGAATTCTTACTAATACAAGAGATATTTTCAACAATACCAGCCATAT
                                                                                                                                                                                                                                                                                                                                                        CTACAGGACATGATTAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                        cracaggacargarragagagarrirircacaargarririrccracrcrirircrgrigit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACATACTTGGAATCAAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTAT
                                                     Gaps
                                                 32;
                                                   Indels
Score 423.4; Db ',
No. 2.4e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis SR;
                                 Pred. No. 2.46
0; Mismatches
                                                                                     CIGGACICCACCAAAIAIGAAGAICIITAICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glenn M, Grigor MR, Molenaar AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine mammary tissue cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCAAGCATAAAAAAAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCAAGCATAAAAAAAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1999; 99US-0150330D.
29-OCT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX11394 standard; cDNA; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-2002; 2002US-00079754
                                   al Similarity 93.4%;
466; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
```

```
The invention discloses isolated histatin polymucleotides and polypeptides, which comprise sequences expressed in bovine. Histatins are histafine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the oral cavity and have promise as therapeutic agents in humans with oral candidosis. Also disclosed are compositions comprising the histatin polypeptide or polymucleotide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The histatin polymucleotide, as useful for treating (e.g. gene therapy) a disorder in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is useful in genome mapping, physical mapping or in the positional cloning of genes. Specifically, the polypeptide or polymucleotide is also useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vaginal, urethra, ear. skin, respiratory tract (e.g. cystic fibrosis systemic infections such as systemic Candida infection. The polypeptide or polymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is the bovine mammary tissue converted specific sequences presented is the bovine mammary tissue converted to the converted converted to the converted converted to the mammary converted to the converted converted to the mammary tissue converted converted converted to the mammary tissue converted converted converted to the mammary converted
                                                                              New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 267 BP; 89 A; 59 C; 43 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.5%; Score 238.4; DB 7;
99.6%; Pred. No. 8.9e-42;
tive 0; Mismatches 1;
                                                                                                                                                                                                                              Example 2; Page 15; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX11390 standard; cDNA; 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.6
Matches 239; Conservative
                                                                                                                                            e.g. infections of the systemic infections.
                            WPI; 2003-275306/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
ABX11390
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
```

```
ö
                                                                            197
                                                                                                                                                        257
                                                                                                                                                                                                                                                                                                                              AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 317
                                                                                                                                                                                                                                                      TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTCACAA 377
                                                                                                                87
                                                                                                                  CAGGACTCCACAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                      CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAAACATCATAG
                                                                            CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                      Gaps
                                    0;
DB 7; Length 267;
                                      Indels
```

```
Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial.
                                                                                      Bovine histatin like polypeptide, #3, cDNA.
                                                           (first entry)
                                                           01-MAY-2003
                              ABX11390;
SXEXEXEX
```

RESULT

taurus

Bos

ó

```
polypeptides, which comprise sequences expressed in bowine. Histatins are histidine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the card cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral candidosis. Also disclosed are compositions comprising the histatin or polypeptide or polymentoeotide, and at least one component consisting of physiological or plarmaceutical carriers or immunostimulants. The comprising the polypeptide, particularly microbial or fungal infections. The histatin polymucleotide is useful for treating (e.g. gene therapy) a comprising the polypeptide, is useful for treating (propertion). The positional cloning of genes. Specifically, the mapping or in the positional cloning of genes. Specifically, the conjugation or polymucleotide is useful for treating fungal or bacterial conjugations or in the positional cloning of genes. Specifically, the conjugation or polymucleotide is useful for treating fungal or bacterial conjugations of the oral cavity (e.g. dental caries, plaque or tartax), caused by Resudomonas acruginosa, mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polymeptide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine conjugation in the polymeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAAACATCATAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cagaacrecaccaaarargaagarcrrrarcrrrarcrrcarrargacrecrcarccrage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses isolated histatin polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB 7; Length 869;
Pred. No. 2.9e-15;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 869 BP; 282 A; 157 C; 147 G; 283 T; 0 U; 0 Other;
                                                                             /product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                              Molenaar AJ, Davis
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 12; 17pp; English
                                                                                                                                                                                                                                           23-AUG-1999, 99US-0150330D.
29-OCT-1999, 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                        19-FEB-2002; 2002US-00079754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.4%;
Matches 121; Conservative (
                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 AGGATATTTTC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTATTCCTC 186
                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                              Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-275306/27.
P-PSDB; ABG75793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systemic infections.
                                                                                                                        US2002164625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176
                    Key
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
```

```
New histatin polynuclectides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                     Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial.
                                                                                                                                                                                     product= "Histatin like polypeptide"
'partial
'note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                          Davis SR;
                                                         Bovine histatin like polypeptide, #5, cDNA.
                                                                                                                                                                                                                                                                                                                                                          Molenaar AJ,
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 12; 17pp; English.
 ABX11392 standard; cDNA; 96 BP.
                                                                                                                                                                                                                                                                                      23-AUG-1999; 99US-0150330P.
29-OCT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00649190.
77-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                   19-FEB-2002; 2002US-00079754
                                                                                                                                                                                ď
                                        (first entry)
                                                                                                                                                                     ....96
*tag=
                                                                                                                                                                                                                                                                                                                                                           Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-275306/27.
                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABG75795
                                                                                                                                                                                                                               US2002164625-A1.
                                        01-MAY-2003
                                                                                                                                                                                                                                                  07-NOV-2002
                                                                                                                                       Bos taurus
```

The invention discloses isolated histatin polymucleotides and polypeptides, which comprise sequences expressed in bovine. Histatins are polypeptides, which comprise sequences expressed in bovine. Histatins are histatine and spart of the non-immune defence system, particularly in the coral cavity and have promise as therapeutic agents in humans with oral cardidosis. Also disclosed are compositions comprising the histatin polypeptide or polypeptide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The comprising the polypeptide, is useful for the composition of discret in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful in genome mapping, physical or polymucleotide is also useful for treating fungal or bacterial mapping or in the positional cloning of genes. Specifically, the mapping or in the positional cloning of genes. Specifically, the collections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or polymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine the control or polymore presented is a cDNA encoding a bovine control or c

Sequence 96 BP; 33 A; 25 C; 10 G; 28 T; 0 U; 0 Other;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GAATITICATGITICATGACTGGACTCCACCAAATATGAAGATCITTATCITTGICAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 GACTCTCTCTTGAGAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTAGT 107
                                                                                                                                                                                                                                                                                                                                                                                   Human, secreted protein, expressed sequence tag, EST; haematopoiesis; tissue growth, activin, inhibin, chemotaxis, chemokinesis, haemostatic; receptor, ligand, thrombolytic; anti-inflammatory, cadherin, anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EST). The
                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliocating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haematocopy activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for
                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from e.g.
                                                                265 TITCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTT
                                                                                              1 TTTCAACAATACCAGCCATATGAACGATATCCACTAAATTATCCTCCTGCGTATCCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynuclectides encoding human secreted proteins - derived fr
human blood, kidney, foetal lung, placenta, testes, brain, ovary,
pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Score 75.4; DB 2; Length 357; 59.4%; Pred. No. 7.6e-07; .ive 0; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 357 BP; 101 A; 74 C; 65 G; 117 T; 0 U; 0 Other;
Length 96;
                                5; Indels
                                                                                                                                   325 CCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                 S
DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Racie LA,
 Score 87; DB 7;
Pred. No. 2e-09;
                                                                                                                                                                   retradadecreeringed
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobs K, Mccoy JM, Lavallie ER,
Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 245; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US006955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00838821.
     14.4%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.4%;
Matches 149; Conservative
                                                                                                                                                                                                                                                       AAV89526 standard; cDNA; 357
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC.
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-070077/06.
 Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                            EST clone CP294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9845436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy
                                                                                                                                                                                                                                                                                                                         15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998.
                                                                                                                                                                                                                                                                                          AAV89526;
                                                                                                                                                                         61
                                                                                                                                                                                                                       RESULT 8
AAV89526
                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                       g
                                                                                                                                         ð
```

239

```
110 crrescricreargarrecerearrascecrearrecerearasasasasascareares 169
                                    180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                  240 ACGGAAAAAACATCAT 255
                                                                                                        170 TAGAAGAAAATTCCAT 185
                                                                                                                                                                                                             21-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                24-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bejanin S,
               20
                                                                                                                                                                                       ABZ36590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                    ð
                                                         g
                                                                                 ò
                                                                                                       g
                                                                                                                                                                ઠે
                                      167
                                                            299
                                                                                                                              281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel human GENSET coding sequences ACC51060-ACC51115) and proteins (ABR46453-ABR48589). The GENSET sequences are useful for preparing a composition for treating GENSET related disorders. They can also be used as markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on Southern gels, as chiromosome markers or tags to identify chromosomes, and as reagents in assays to quantitatively
                                                            240 ACGCAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                                    crredericreargarrecardarradedecrearreacardaaaadadacardardedera
                                                                                                        300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                              222 GGACTGTGGATCAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
                                                                                  -----GAAAAGCATCATTCACATCGAGAATTTCCATTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New GENSET polynucleotides and polypeptides, useful for preparing a composition for treating GENSET-related disorders and as reagents in assays to quantitatively determined levels of GENSET expression in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determined levels of GENSET expression in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 70.4; DB 7; Length 438;
69.9%; Pred. No. 9.3e-06;
iive 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 438 BP; 155 A; 80 C; 60 G; 143 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Human; GENSET; therapeutic; therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 404-405; 505pp; English.
                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                        Human Chimerin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2001; 2001US-0293574P.
15-UUN-2001; 2001US-0298698P.
29-UUN-2001; 2001US-0302277P.
13-UUL-2001; 2001US-0305456P.
                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-2001; 2001WO-IB001715
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                 168 TAGAAGAAATTCCAT
                                                                                                                                                                                                                                   ACC51062 standard; cDNA;
                                                                                                                                                                          282 TATAGAGGTTT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-129412/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABR48455
                                                                                                                                                                                                                                                                                                                                                                           WO200294864-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                  13-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ś
                                    108
                                                                                                                                                     360
                                                                                                                                                                                                                                                          ACC51062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bejanin
                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                     d
                                                         8
                                                                              셤
                                                                                                        ò
                                                                                                                            ద
                                                                                                                                                    à
```

```
The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New GENSET polymucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GAATTICATCTITCATGACTGGACTCCACCAAATATGAAGATCTITATCTITGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TAIGGCICTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                       Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 70.4; DB 7; Length 438; 69.9%; Pred. No. 9.3e-06; tive 0; Mismatches 41; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 438 BP; 151 A; 80 C; 60 G; 145 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                                             Human GENSET coding sequence SEQ ID 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 478; 735pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,0
ВР
   CDNA; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2001; 2001WO-IB000914
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-075548/07.
ABZ36590 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200283898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

ö

Gaps

. 0

120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179

Conservative

Best Local Similarity Matches 95; Conserv

à

```
RESULT 12
                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel GENSET polynuclectides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 criedcicicarcarantrecarantradederrearrearandadacareareda 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTICAICITICAIGACTGGACICCACCAAAIAIGAAGAICITIAICITIGICITICAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           so gacticicititgagiaaaggacitggccaactaigaagriritigicitifgcrifagi
                                                                                                                                                                                                 Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 438 BP; 153 A; 80 C; 60 G; 143 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Jobert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 11.7%; Score 70.4; DB 7; 1 Similarity 69.9%; Pred. No. 9.3e-06; 95; Conservative 0; Mismatches 41:
                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                           Human GENSET coding sequence SEQ ID 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 295; 735pp; English.
                                                                                                     ABZ36425 standard; cDNA; 438 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 TAGAAGAAAATTCCAT 185
               240 ACGGAAAAAACATCAT 255
                                         170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                          18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                  18-APR-2001; 2001WO-IB000914.
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Bejanin S, Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-075548/07
                                                                                                                                                                                                                                                                                           WO200283898-A1
                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                    21-FEB-2003
                                                                                                                                                                                                                                                                                                                  24-OCT-2002
                                                                                                                             ABZ36425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                            RESULT 11
                                                                                           ABZ3642
                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \delta
                                         g
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GATTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTTGTTTTTTGCTTTAAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TAIGGCICTCAICCIAGCCAIGAITAGAGCTGAITCAICTGAAGAGAAAGGICACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 criedcicicarecirricalidaciedadcidarircacaidcaaadadacaicardddia 480
                                                                                                                                                                                                   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asundi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 857 BP; 231 A; 194 C; 169 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%; Score 68.2; DB 4; Length 8 65.4%; Pred. No. 3.1e-05; Live 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen R,
                                                                                                                                                                   Human EST-derived coding sequence SEQ ID NO: 515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAACATCATAGAGGATATTTTCAACA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n XB, Wang Z,
Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 TAAAAGAAATTCCATGAAAAGCATCATTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ou P, Qian XB,
Zhang J, Werhr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 537; 1275pp; English.
                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00491404.
2000US-00617746.
2000US-00631451.
2000US-00663870.
                     AAH98658 standard; cDNA; 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001; 2001WO-US002687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA48964 standard; DNA; 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P,
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476164/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAM23999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention
                                                                                                                                                                                                                                                                                                                                                                                                   WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2001.
                                                                                                                        12-OCT-2001
                                                                        AAH98658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
AAA48964
ID AAA48
XX
AAH98658
```

```
239 AATACCAACAATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-663472/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ADE40262
                                                                                                                                                                                                                                                                                                                                                                                            WO2003064589-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001;
17-AUG-2001;
17-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-Aug-2001;
20-Aug-2001;
21-Aug-2001;
23-Aug-2001;
29-Aug-2001;
29-Aug-2001;
17-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-2001;
05-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2002;
07-JUN-2002;
                                                                                                                                                   29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smithson G;
                                                                                                                     ADE40261;
                                                    RESULT 14
                                                                  ADE40261
유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human lysine-rich statherin protein (LRSP) (AAY94526). The CDNA sequence encoding this protein was identified through analysis of a CDNA library of breast tumour tissue (BRSTNOT14). The LRSP sequence was found to have homology with the DNA of human statherin (the present sequence) and human basic histidine-rich protein (AAY94528). Human statherin is a phosphoprotein that acts as an inhibitor of precipitation of calcium phosphate salts in the oral cavity. The LRSP polypeptide and its antagonists may be useful for treating or preventing disorders associated with the activity of LRSP. Such disorders include autoimmune/inflammatory disorders (for example AIDS, allergies, asthma, diabetes mellitus), bacterial and fungal infection and cancers (such as leukemia, adenocarcinoma, melanoma). Antibodies to LRSP may be useful for diagnosis of the above disorders
                                                                                                 Lysine-rich statherin protein; LRSP, acidic phosphoprotein; human; precipitation inhibitor; autoimmune; inflammatory disorder; AIDS; asthma; allergy; diabetes mellitus; fungal; bacterial infection; cancer; leukemia; adenocarcinoma; melanoma; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTATATGGCTCTCATCCTAGCCA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATCTTGGCTCTCATGGTTTCCA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATTGGAGCTGATTCATCTGAAGAGAAATTTTTGCGTAGAATTGGAAGATTCGGTTATG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derandecertrancaeccaerrecaeaccaerrancecaecaeccaraeccaeccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 GATA-----TTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified polypeptide used for treating or preventing a disorder characterized by expression or activity of lysine-rich statherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               о
О
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 67.6; DB 3; Length 552; 61.2%; Pred. No. 3.8e-05; cive 0; Mismatches 84; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 552 BP; 172 A; 122 C; 78 G; 180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patterson
                                                                                                                                                                                                                                                       /*tag= a
/product= "Statherin"
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 71; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                           98US-0155209P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.2%;
Matches 147; Conservative
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350699/30.
P-PSDB; AAY94527.
                                                                  Human statherin DNA
                                                                                                                                                                                                                                                                                                         WO200024779-A1
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                  06-OCT-2000
 AAA48964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                        Key
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
                                                                                                                   antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AlDS; multiple sclerosis; graft-versue-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman X, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
BP.
                                                                             Human NOV38a cDNA - SEQ ID 167
                                                                                                                                                                                                                                                                                                                                                         200105-0310951P

200108-0312892P

200108-0312892P

200108-0313415P

200108-0313415P

200108-0313403P

200108-0313403P

200108-0314031P

200108-0315403P

200108-0315403P

200108-0315403P

200108-0315403P

200108-0315403P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0340233P.
2002US-0354591P.
2002US-0365478P.
2002US-0373814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0373825P.
2002US-0373989P.
2002US-0374632P.
2002US-0386971P.
ADE40261 standard; cDNA; 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacogenomics.
```

```
2,
                                     The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytoscatic, ancrectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and synaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, preventing NOVX-associated disorders including cardiomyopathy, atheroscierosis, hypertension, cancer, obseity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Askhison's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV CDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATA-----TITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 aaraccaacaararacrittraararcarcacagraacrigcaggacargarrarrgaggcrit 495
                                                                                                                                                                                                                                                                                                                                                                                                                                   315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     256 GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATCTTGGCTCTCATGGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAAACATCATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, ss, gene, pharmaceutical, diagnostic, gene thérapy, tissue régeneration, cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein, osteoporosis, neurological disease; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                            5; DB 9; Length 678;
4e-05;
ches 84; Indels
                                                                                                                                                                                                                                                                                         Sequence 678 BP; 190 A; 151 C; 137 G; 200 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Clone SALGL10001070 protein"
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                            Score 67.6;
Pred. No. 4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding clone SALGL10001070
              Claim 20; SEQ ID NO 167; 560pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
89. .997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB63039 standard; cDNA; 1584 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                              / Match 11.2%;
Local Similarity 61.2%;
les 147; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376
                                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB63039
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB63039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide or the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide or is useful as a primer for synthesising the polynucleotide in an expressible manner for synthesising the polynucleotide or as a probe conformant carrying the polynucleotide or as a probe conformant carrying the polynucleotide or as a probe conformant carrying the polynucleotide and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or conformant or regeneration. Membrane proteins, isgnal transduction-related proteins, isgnal transduction-related proteins, disease-related proteins or encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for diseases (e.g. osteoporosis, encoding them can be used as indicacors for disease (e.g. osteoporosis, encoding them can be used as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1083 GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATGTTTGGCTTTCATGGTTTCCA 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1263 AATACCAACAATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATA-----TITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT 370
      Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                               New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 TGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAAACATCATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1143 İCATIGGAĞCTGATTCATCTGAAGAAAATTTTTGCĞTAGAATTGGAĞATTTCGĞTTATĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ص
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
11.2%; Score 67.6; DB 9; Length 1584;
Best Local Similarity 61.2%; Pred. No. 4.6e-05;
Matches 147; Conservative 0; Mismatches 84; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1584 BP; 526 A; 298 C; 331 G; 429 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 15, 2004, 21:45:07 Job time : 355 secs
                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 222pp; English
                      Sugiyama T,
                                                  Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                            WPI; 2003-450961/43.
P-PSDB; ADB65009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 (
                         Isogai T,
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
518770 ACTATATCCACAATTTCAAATAAAGAT 518797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-790-988-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-09-790-988-1
                              шимши имини

шимши имини

шими имини

шим
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                0000 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \stackrel{\sim}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Applisequence 28, Applisequence 39, Applisequence 197, Applisequence 197, Applisequence 29, Applisequence 29, Applisequence 29, Applisequence 21, Applisequence 214, Applisequence 214, Applisequence 214, Applisequence 214, Applisequence 26, Applisequence 26, Applisequence 214, Applisequence 26, Applisequence 27, Applisequence 26, Applisequence 26, Applisequence 26, Applisequence 5, Applisequence 6, Applisequ
                                                                                                                                                                                                 August 15, 2004, 21:39:53 ; Search time 73 Seconds (without alignments) 4591.648 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gaagtattttcagttctata......tatcaagcataaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549650-7

US-08-973-462-1

US-09-702-712-214

US-09-614-124B-214

US-09-671-323-214

US-09-671-323-214

US-09-671-323-214

US-09-671-323-214

US-10-204-708-84

US-10-204-708-84

US-09-417-4850-7

US-09-417-4850-5

US-09-417-4850-5

US-09-417-4850-5

US-09-417-4850-5

US-09-417-4850-5

US-09-417-4850-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-110-204-708-28
US-110-204-708-38
US-10-204-708-39
US-09-468-265-4
US-09-265-197
US-10-204-708-74
US-09-367-895-29
US-08-991-803-29
US-08-991-462-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                           using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5496550-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-4
604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0 640681
6.9 11131
6.9 15501
6.9 19513
6.8 18613
6.8 11478
6.8 11478
6.8 11478
6.8 11478
6.9 11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                               nucleic search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match 1
                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

```
Sequence 2813, Ap
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 2706, Ap
Sequence 2, Appl
Sequence 19, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
                                                                                                                                                                      Sequence 3 Sequence 3 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                            Sequence
US-09-621-976-2813

US-08-487-826-813

US-08-487-826-13

US-08-487-826-13

US-09-543-681A-2706

US-09-543-681A-2706

US-08-817-926-19

US-08-187-926-19

US-08-187-926-19

US-08-184-632-1

US-08-184-632-1

US-10-204-708-2

US-10-204-708-18

US-09-527-122-11

US-07-867-106-2

US-10-204-708-18

US-09-627-122-21

US-09-627-122-21

US-09-627-128-18

  832 4
832 4
19124 2
1664976
19124 2
```

ALIGNMENTS

```
518710 TTATATCCATCAAGATGAAGATAAAAAAAAAATATTTTGAATATTTCTGTAATTTACGA 518769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518530 TATAAAATTAGAAAACAACTAAAATTAATGGTTTTAGAAAAGGAAAAACTCCTATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 GATCTTTATCTTTGTCTTCATTATGGCTCTCGTCGTAGCCATGATTAGAGCTGATTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AGAACATCTCCTGAAGCATCAGAATTTCATCTTTCATGACTGGACTCCACCAAATATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518590 AGTAATACAAGAAAGTATGGTAGTGCTATTTATTATGATATTTTAAAAAACTAATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 IGTAATTACAAAACAAATGAAGGATTTCAAGGTATTTAAACACAGGAGTTTTCTAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAATACCA
Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INPORMATION; SHUJI
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: HATANABE, HIDEMI
; APPLICANT: HATANABE, HIDEMI
; APPLICANT: GENERAL PROBLYMER
; TITLE OF INVENTION: GENERAL DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REPRENCE: 081356/0159
; CURRENT APPLICATION NUMBER: UP2000-107160
; RICH FILING DATE: 2001-02-23
; PRIOR FILING DATE: 2001-04-07
; NUMBER OF SEQ ID NOS: 7
; SOSTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 640681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 42.4; DB 4; Length 6 47.4%; Pred. No. 1.8; tive 0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 GCCATATCAACGATATCCACTAAATTAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.4
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 640681
```

```
9025 TAACTAATAATCTATTAATAAATAACAACTTCCTCAATAACTTTATAAATTTTACTTT 8966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8965 caahtaraccrcaarcarrirhaacaachaarrarchaaacccaaarcccrarcaaaraar 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8905 aaairraacraraaaarraacraaraacrcarraaaaaracaaarrirraaaccaaa 8846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8845 acriccaaaaarrcraarriraararraraaaccrraaaarccararaaarraaaarrir 8786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACTTT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent NO. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEBENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTCTCTGTCACTTACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAA 600
                                                                                                                                                                                                                           244 AAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAAT
                                                                                                                                                                                                                                                                                424 GAATAAAAGAAAGAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAA
                                                                                                                                                                                                                                                                                                                                  304 INTCCTCCTGCGINICCATTTCCTTAAANGCTGCTTAGTAACTACAGGACATGATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                         364 GAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGTTGAAAACCATCTTTCAAAT
                                                                                                                       Length 11131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.8%; Pred. No. 0.82;
Matches 105; Conservative 0; Mismatches 106; Indels
                                                                                                                                                                               Indels
                           ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA
US-10-204-708-28
                                                                                                                          Query Match
6.9%; Score 41.8; DB 4;
Best Local Similarity 44.8%; Pred. No. 0.8;
Matches 160; Conservative 0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR PELING DATE: 2003-06-06
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/10204708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-204-708-38/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220644 GITACCCAGGAATGCTCGATTGCTTCATTAAAGCTAATCCTAATTTTTTCATCATATGA 220585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220764 Tracgridadahaahredachacgridricarrahahadarcarcargrahradage 220705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diseases Associated with DNA Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 GATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGAAAACCATCTTTCAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220704 TCTTTTCAATATTTCCATTTTCTACTTTTTTTTTCAGCGTTTTCTATTGTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAAAACAAAAAAAAAAATCAGTCAAGTAGTTGCACAAAAACATACTTGGAATCAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 TCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 640681;
                                                                                                                               APPLICANT: HATTOR! MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REPERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR TELING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-204-708-28/5

US-10-204-708-28/6/5

Patent No. 6677731
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.2; DB 4;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220584 ACAATTTTATCAGACGCAAAAT 220562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 TCAATATTTTAAAACATAATAAT 508
             Sequence 1, Application US/09790988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.55
Matches 125, Conservative
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                       WATANABE,
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-204-708-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 28
LENGTH: 11131
TYPE: DNA
                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                 Gaps
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-38
                                                                       Length 5501;
```

us-10-0/9-/54a-4.rui

GABREAL INFORMATION:

APPLICANT: Barka, Mahalel

APPLICANT: Cullen, Daniel

APPLICANT: Cullen, Daniel

APPLICANT: Cullen, Daniel

APPLICANT: Gregory L

APPLICANT: Hayenga, Kirk J

APPLICANT: Davie, Virgil B

TITLE OF INVENTION: Making Same and Vectors for Making Same

FILE REFERENCE: A-42903-5

CURRENT APPLICATION NUMBER: U8/09/468,265

CURRENT FILING DATE: 1994-08-02

PRIOR FILING DATE: 1994-08-02

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1985-08-29

NUMBER OF SEQ ID NOS: 28

SOFTWARRE: ParentIn Version 3.1

SEQ ID NO 4-4

```
US-LY-CAG-1/08-397/C
Sequence 30, Application US/10204708
Fatent No. 6677731
GENERAL INFORMATION:
FAPPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013-1012
CURRENT PELICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 100132529.7
FRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9568 AACCAAAATCGCACCACTATACTCCAACCTAAATAACAAAACTCCGTCTCAAAA 9509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1921 ATAAAATTAAAAAATATATAAACAAAAAAACTAAAACAAATCAAATAAAA 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 AACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAAC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 AACGTCACAGGAAACGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 TACAGGACATGATTAGGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTG 406
TAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGTGAAAACCATCTTTC 419
                                                                                                                                          AAATGAATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACACATACTTGGAAT '479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 6.9%; Score 41.4; DB 4; Length 19513; Best Local Similarity 46.9%; Pred. No. 1.2; Matches 129; Conservative 0; Mismatches 146; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTABATABACATABACABATABABTATCATA 9354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 ACATACTIGGAATCAAATATCAATATTTTAAAACA 501
                                                                                                                                                                                                                                                                                                                                                                              1861 TAAAATATAAAAATAATAAAATAATCA 1831
                                                                                                                                                                                                                                                                                                     480 CAAATATCAATATTTTAAAACATAATGA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-204-708-39/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \dot{\delta}
                                                                                                                                                  ò
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                     \delta
```

셤 Š

281 CATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTT

221 AAGAGAAACGTCACAGGAAACGGAAAAAAAACATCATAGAGGATATTTTCAACAATACCAGC

Query Match 6.8%; Score 41.2; DB 4; Length 1 Best Local Similarity 46.3%; Pred. No. 0.68; Matches 136; Conservative 0; Mismatches 158; Indels

, ORGANISM: Emericella nidulans US-09-468-265-4

TYPE: DNA

Length 1864;

```
1344 AAGAATITAATIAATITAAATATATATATATATATATATGTTGACCITGAAACTGTTACTAAA 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1284 AACTGAATAATATTAAAGAATAGTATTATCTAAGTATAACTTAAATCTTAGTAATACTA 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 197, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Cocks, Benjamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES. 1508
                                                                                                                                              341 AGTAACTACAGGACATGATTAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                     1464 TAAAAATAGTCTAGGAGAATAATAAAGCTCTATAAAAAATTATTAAGATTATT 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 CACAACACATACTTGGAATCAAATATCAATATTTTTAAAACATAATAATGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-023-655-197/c
       g
                                                                                                                                              ò
                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
```

RESULT 6 US-09-468-265-4

```
generic 29, Application US/09367895

Faquence 29, Application US/09367895

GENERAL No. 643009

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

FILE REPRESENCE: 076883/0112

CURRENT APPLICATION NUMBER: US/09/367,895

CURRENT APPLICATION NUMBER: US/09/367,895

CURRENT FILING DATE: 1999-12-08

FRIOR FILING DATE: 1999-12-08

FRIOR FILING DATE: 1998-0220

FRIOR PRILING DATE: 1998-02-21

FRIOR FILING DATE: 1997-03-24

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PALENTH OF NOS: 43

SOFTWARE: PALENTH OF NOS: 43

SEQ ID NO 29

LENGTH: 11469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11372 iritgacarcritricigiraraarritririritritraaraacaacaacaaga 11313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4931 irtababanahribacerahannahaharrentrahacahahanahaharahahrene 4872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 TITITICACAATGATITITICCTACTITITICTGTTGTAAAAACCATCTTTCAAATGAAT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 AACACATACTTGGAATCAAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              ; FEATURE:
*, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 4; Length 11469;
Pred. No. 1.3;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 4; Length 5152;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LOCATION: (2132..2209, 3375..3494, 3812..4033, 4538..4606, LOCATION: 4753..5022, 5241..6146, 6345..6461, 6670..6732, LOCATION: 7026..7133, 7510..7611, 7784..7852, 7998..8078, LOCATION: 8321..8437, 9235..9630)
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 100;
PRIOR FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4751 TAATAATCCATAAAACCAAAA 4731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584 CTATCAAGCATAAAAAAAA 604
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                           6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%;
ilarity 51.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.2
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-367-895-29/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jequence 74, Application US/10204708

Jequence 74, Application US/10204708

Jetent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPRNBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: DASSessing DNA Methylation

TITLE OF INVENTION: DASSessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06

PRIOR PILING DATE: 2003-06-06

PRIOR FILING DATE: 2003-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PLILICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 ACATTGATAAGAATGATGTTTAACAATTTTTTTGAAAATAAAATAAACCCTATATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 TTTAGTAAAAAAAAAAAAATATAAATGCTCTTTGCAAAGACCACCATTCATAAAATT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 GTAAATATTTTGTATGTCAATTTCTGACATCCTTTTTTACTGGGTAATTTCTGTTTTTATGC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 AGAITITICACAAIGAITITICCIACICITICIGITIGAAAACCAICITICAAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 AATAAAACAAAGAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERRNCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
LELECOMMUNICATION INFORMATION:
LELECOMMUNICATION OF SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 Dasse pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No. 0
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIEN: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95; Conservative
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: THP1PEB01
CLONE: 073582
US-09-023-655-197
             CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 CGTTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .10-204-708-74/c
                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545
               STATE:
```

```
SEQ ID NO 29
LENGTH: 11478
                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11381 Thigacarcritricigirahaarritricirricratrakakaacaacaacaadaka 11322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11321 AAAACAATGAAGAAATCAATAGAAAGGGAAGAATTTTCATACTCATTTGAAAGCGAA 11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11261 AATCTACTAGAAGAAGATGATGATGAACTCTTGAAACTTTCATTAGTGACACCCTTGGTT 11202
                                                                   11312 AAAACAATGAAGAAATCAATAGAAAAGAGGAAGAATTTTCATACTCATTGAAAGCGAA 11253
                                                                                                                                                      11252 AATCTACTAGAAGAAGATGATGAACTCTTGAAACTTTCATTAGTGACACCCTTCGTT 11193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 TITITCACAATGATITITICCTACTCTTTCTGTTGAAAACCATCTTTCAAATGAAT 427
                             428 AAAACAAAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.8%; Score 41; DB 3; Length 11478;
Best Local Similarity 51.4%; Pred. No. 1.3;
Matches 95; Conservative 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHEBITION OF GENE EXPRESSION
FILE REPERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-14
EARLIER APPLICATION NUMBER: 9514435.8
EARLIER FILING DATE: 1996-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENT UST: 200
SEQ ID NOS: 31
LENGTH: 11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRUERAL INC. 021201.

APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRES
TITLE REFERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1995-07-14
SARLIER FILING DATE: 1995-07-15
SOFTWARE: PALENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/08983440 Patent No. 6232122
                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-981-803-29/c
; Sequence 29, Application US/08981803
; Parent No. 6147279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA CRGANISM: Solanum tuberosum US-08-981-803-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11201 CTAČT 11197
                                                                                                                                                                                                                                                11192 CTACT 11188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 TCTCT 552
                                                                                                                                                                                                     548 TCTCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-983-440-29/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                  ò
                                                                                                                                                             g
                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                              g
```

```
11321 AAAACAATGAAGAAAATCAATAGAAAAAGAGGAAGAATTTTCATACTCATTTGAAAGGAA 11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11261 AArcracragaagangargargargacricrrgaagcriricarragragagaccrirgir 11202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11381 Thigacarchtricterrataaartiticirictriticaataacaacaacaataaa 11322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 ITITICACAAIGAITITICCIACICITICIGITGIGIAAAAACCAICTICAAAIGAAI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DAUGHES, PIERRE
APPLICANT: DAUGHES, PIERRE
APPLICANT: DAUGHES, PIERRE
APPLICANT: DAUGHES, PIERRE
TITLE OF INVENTION: MALARIAL, PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 AAAACAAAAAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 AATATITIAAAACATAAIAAIGATAGICCICIGAACTAIGIAAITGGTITCTACTITCTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.8%; Score 40.8; DB 3; Length 6152;
Best Local Similarity 53.0%; Pred. No. 1.2;
Matches 87; Conservative 0; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 41; DB 3;
51.4%; Pred. No. 1.3;
                                                                                                                                                                        or C or T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or T/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: variation
LOCATION: (1)..(11478)
CTHER INFORMATION: M stands for A or
US-08-983-440-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OĽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-973-462-1
Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
                                                                                                                                                                                                                        FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
LOCATION: RIFORMATION: R stands for G
FEATURE:
NAME/KEY: variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: variation
NAME/KEY: variation
OCATION: (1)..(11478)
OTHER INFORMATION: W stands for A
FEATURE:
                                                                                      NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: B stands for G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(11478)
OTHER INFORMATION: K stands
ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.4'
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA; ORGANISM: P. falciparum US-08-973-462-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11201 CTACT 11197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 TCTCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6152
```

us-10-079-754a-4.rni

```
, LENGTH: 466
5496550-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-973-462-1/c
SEQ ID NO:7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search cor
Job time
                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                    AAATGAATAAAACAAAGAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAAT 479
                                                            309 дадададададададададададатскасстататаспататдтатдатататататата 368
                                                                                                                                          425 AATAAAACAAAGAAAAAAAAATCAGTCAAGTAGTTGCACAACACACATACTTGGAATCAAAT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 ATCAATATTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACTTTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 ITTICTCTGTGACTTACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAAAA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 GIGICITIGICGAITCAIGIGCAIGCAIATICACITCAAAAAGCCCGCAAAAATAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
SOCYSTS FROM A NEWBORN CHICK
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/108,763
FILING DATE: 17-AGG-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 42,219
FILING DATE: 14-FBB-198
APPLICATION NUMBER: 15,63
FILING DATE: 12-FBB-198
APPLICATION NUMBER: 15,245
FILING DATE: 12-FBB-198
APPLICATION NUMBER: 15,245
FILING DATE: 12-FBB-198
APPLICATION NUMBER: 15,245
FILING DATE: 14-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARABLE OF THE NUMBER: 15,245

MUMBER OF SEQUENCES: 10

CURRENT APPLICATION DATE: 10/08/108,763

FILING DATE: 17-AUG-1993

PRIOR APPLICATION NUMBER: 42,219

FILING DATE: 16-JAN-1991

APPLICATION NUMBER: 310,603

FILING DATE: 14-FEB-1989

PILING DATE: 12-FEB-1989

PILING DATE: 11-FEB-1989

PILING DATE: 12-FEB-1989

PRELICATION NUMBER: 310,603

FILING DATE: 11-FEB-1989

PILING DATE: 11-FEB-1989

PILING DATE: 11-FEB-1989

PILING DATE: 11-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 465;
                                                                                                                                                                                       540 CTTTCTTTTCTCTGTCACTTACCATGCATGCTTAATAAATTGAT 583
                                                                                                                                                                                                                             429 TATTATCTTTTAGTCTGATATAACAAGAGTTGGAAAAAAA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.4; DB 6;
Pred. No. 0.71;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 896,611
FILING DATE: 14-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.7%;
Matches 92; Conservative C
                                                                                                                                                                                                                                                                                                                                      5496550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                    , Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
5496550-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5496550-9
                                                                                                                                                                                                                                                                                                                5496550-9
                                                     g
                                                                                                  \delta
                                                                                                                                          셤
                                                                                                                                                                                   \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
ö
                                                                                                425 AATAAAACAAAGAAAAAAAAAATCAGTCAAGTAGTTGCACAACACACATACTTGGAATCAAAT 484
                                                                                                                                           480 CAAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTA 539
                                                                                                                                                                                              485 ATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACTTTC 544
                                                                                                                                                                                                                                       APPLICANT: DRUBLES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PERFERENTIAL OF PREPRICE STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT PILLING DATE: 1996-02-06
BARLIER APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/973,462B
BARLIER APPLICATION NUMBER: PCT/FR96/00894
BARLIER PILLING DATE: 1996-06-12
BARLIER FILLING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                          545 TITITCTCTGTCACTTACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAAAA 602
                                                                                                                                                                                                                                                                                                                                       270 GIGTCTTTGTCGATTCATGTGCATGCATATTCACTTCAAAAAAGCCCGCAAAAATAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 AAATGAATAAAACAAAGAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAAT
                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6152;
     Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                86; Indels
     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
  Score 40.4; DB
Pred. No. 0.71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.7%; Score 40.2; DE
Best Local Similarity 56.4%; Pred. No. 1.6;
Matches 75; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: August 16, 2004, 00:16:44
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08973462B Patent No. 6191270 GENERAL INFORMATION:
6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 CTTTCTTTTCTCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: P. falciparum
-08-973-462-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 TTTTTTTTTT
  Query Match
Best Local Similarity
Matches 92; Conserv
```

```
(without alignments)
7677.697 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                               1 gaagtattttcagttctata......tatcaagcataaaaaaaa 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
                                                                                                                                                                                                 August 15, 2004, 21:45:13 ; Search time 386 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6451454
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3225727 segs, 2453303834 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapopt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                   US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

<u>.</u>	4,	H	7	6, Appli		200, App	m m	5, Appli	'n	π,	5, Appli	Ŋ	'n	'n
Description	Sequence	Segnence	Seguence	Segnence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
۵I	US-10-079-754A-4	US-10-079-754A-1	US-10-079-754A-2	US-10-079-754A-6	US-10-079-754A-15	US-10-079-623-200	US-10-079-754A-3	US-10-079-754A-5	US-09-992-600A-5	US-09-924-340-5	US-09-992-095B-5	US-09-999-570-5	US-10-000-489-5	US-10-000-986-5
	14	14	14	14	14	14	14	14	10	10	10	10	15	15
% Query Match Length DB	604	505	585	525	267	267	869	96	438	438	438	438	438	438
% Query Match	100.0	77.1	74.2	70.1	39.5	99. 5	19.0	14.4	11.7	11.7	11.7	11.7	11.7	11.7
Score	604	465.4	448.2	423.4	238.4	238.4	115	87	70.4	70.4	70.4	70.4	70.4	70.4
Result No.		C)	m	4	Ŋ	9	7	00	6	10	11	12	13	14

· 0

1 GAAGTATTTTCAGTTCTATAATAAGATCTCATAACTGATGTAATTACAAAAACAAATGAA 60

d \ddot{o}

5,		e 16	Seguence 1193, Ap	e 26	e 2638	638	€ 2638	equence 2636	equence 2636	equence 30	quence 1356	Sequence 2,	934,	271,	quence 381,	Sequence 1,	equence 1453		962	9	2098,	128,	1416	750,	equence 43,	equence 19,	equence 35,	ednence 739,	equence 23	Sequence 74, Appl
US-10-154-678-5	US-10-001-142-5	-10-210-17	US-10-104-047-1193	US-10-027-632-263847	-10-027-63	-10-027-63	-10-027-63	32-26384	-10-027-63	-10-115-635-3	13		10-311-455-9	-10-311-455-27	-10-221-7	US-10-312-841-1	10-311-455-1	-10-311-45	5-9	-10-240-589C-5	-10-311-455-20	-10-240-589C-12	-10-424-599-1	-10-311-455-75	-10-221-714A-	-10-172-086-1	7-3	10-311-45	-10-240-453-23	US-10-240-589C-74
15	15	13	16	13	13	13	16	16	16	17	15	15	15	15	13	15	15	15	12	17	15	17	13	15	13	15	17	15	12	17
438	438	678	1584	1521	1521	1521	1521	1521	1521	457	13449	3673778	6255	12507	12578	3673778	7106	5945	16994	13131	73334	73334	699	6782	6274	6274	6274	19659	6155	6280
11.7	11.7	H	11.2	σ			. :	00		9.6				8.4		8.4	8.2		8.2		8.1						٠		7.8	•
70.4				΄ σ	, σ	. 0	6	59.2	6	28	53.6	ហ	51.2	Ŋ	51	51		σ,	6	9		4		47.8		۲.			47.2	47.2
51	9	17	. cc	9 0	10	2.5	22	23	24	25	26	N	N	N	וחו	m	m	ייי	(*)	(יי)	ניי	(1)	(*)	(*)	4	4	4	4	C 44	c 45

ALIGNMENTS

```
1 GAAGDATTTTCAGTTCTATAATAAGAICTCATAACTGGAGGTAATTACAAAAACAAATGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
             US-LUCIVERY APPLICATION US/10079754A

SQUENCE 4, Application US/10079754A

PUBLICATION NO. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REPERBNCE: 11000-1068

CURRENT APPLICATION NUMBER: US 09/699,146

FRIOR FILING DATE: 2000-10-27

FRIOR APPLICATION NUMBER: US 60,162,701

FRIOR APPLICATION NUMBER: US 60,162,701

FRIOR APPLICATION NUMBER: US 09/644,190

FRIOR FILING DATE: 2000-08-22

FRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 15

SOSTWARE FREEKE FREEK FREEKE FREEK FREEKE FREEKE FREEK FREEKE FREEK 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

100.0%; Score 604; DB 14;

Best Local Similarity 100.0%; Pred. No. 4.9e-128;

Matches 604; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-4
US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 604
```

a

197

87

437

Tue Aug 17 16:21:39 2004

121

181

ò

241

ò

g

à

301 361 421 481 481 541

d

ઠે 셤 ò

421

ò

d

ò

601 601

ò

61 121

g ઠે US-10-079-754A-1

Query Match

197

```
TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAATATCAATATTTTTAA 387
                                                                                                                                                                                             CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGAAAAAACATCATAG 257
                                                                                                                                                                                                                                                                                                              AGGATATITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 317
                                                                                                                                                                                                                                                                                                                                                                                                                               TCCATTTCCTTAAAATGCTGCTTAGTAACTACGACATGATTAGAGAGATTTTTCACAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgaririricciacitriricigirigigirigaaaaccarcriricaaargaaraaaacaaaga 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATCAATATTTAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 CAGGACTICCACCACAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCATGCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATTTTTCCTACTTTTCTGTTGTTTGAAAACCATCTTTCAAATGAATAAAACAAAGA
                                                                               CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 CAGGACTCCACCAAATATGAAGATCTTTATCTTTATCTTCATTATGGCTCTCATCCTAGC
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. Application US/10079754A

Sequence 2. Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Doris, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

TITLE OF INVENTION: NUMBER: US/10/079,754A

CURRENT FILING DATE: 1000.1068

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR PELING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR PELING DATE: 1999-10-29
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.8%; Pred. No. 2.1e-96;
Matches 466; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.2%; Score 448.2; DB 14; Length
99.3%; Pred. No. 1.9e-92;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.3
Matches 450; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-079-754A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                  318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388
                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                    258
                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448
                                                                                                                                                                                                                                              q
                                                                                                                                      đ
                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                     120
                                                                                                                                            180
                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAAGACATGATT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGAATAAAACAAAGAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900
                                                                         GGATTICAAGGTATTTAAACACAGGTTTTTCTAGCAAAGAACATCTCCTGAAGCATCAC
                                                                                                                                                                                 AATTTCATCTTTCATGACTGGACTCCAACAAATATGAAGATCTTTATCTTTGTCTTCATT
                                                                                                                                                                                                                                                                                                                 181 Arggerererereragecargarragagergarrearcregagagagagacereagaga
                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTGAAAACCATCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 AGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTGAAAACCATCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATATCAATATTTTAAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCTTTTCTCTGTCACTTACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 TITCITITICICIGICACTIACAIGCAIGCTIAATAAAITGAICIAICAAGCAIAAAAAA
                                                                                                                                               AATTICATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATT
                                                                                                                                                                                                                                                                                                                                                                           CGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthen J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR PILING DATE: 1299-10-29
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,703
PRIOR APPLICATION NUMBER: US 60,162,703
PRIOR APPLICATION NUMBER: US 60,160,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%; Score 465.4; DB 14; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10079754A, Publication No. US20020164625A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Bovine
```

ò g ò 셤 ò g ò d ò

```
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
                                                                                                                                       405
                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                            525
                                                                                                                                                                                                                                                                                                                                    446
                                                                                                                                                                                                                                                                                                                                                                            585
                                                                                                                                                                                                                                                                                                                                                                                                               506
                                                                                                                                                                          326
                                                                                                                                                                                                                  465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGAAACGAAACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 caddacrecaecaaarardaagarerrrarerrregeerrearrardecretade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                   447 GIAATIGGITICTACITICTTITICTCTGTCACTTACCATGCATGGTTAATAATTGATCT
147 TGATAGGTCTCCAGAATTCTTACTAATACAAGAGATATTTTCAACAATACCAGCCATAT
                                                            CAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAA
                                                                                           CAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAA
                                                                                                                                                                      267 CTACAGGACATGATTAGAGAGATTTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGTT
                                                                                                                                                                                                                  CACATACTTGGAATCAAATATCAATATTTAAAACATAATAATGATAGTCTCTGAACTAT
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                         CTACAGGACATGATTAGAGATTTTTTCACAATGATTTTTCCTACTCTTTCTGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.5%; Score 238.4; DB 14; Length 267; 99.6%; Pred. No. 1.2e-44; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000-11068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR RILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR PILING DATE: 1999-08-22
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 15, Application US/10079754A; Publication No. US20020164625A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 ATCAAGCATAAAAAAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAAGCATAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bovine US-10-079-754A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-079-754A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                286
                                                                                                        207
                                                                                                                                             346
                                                                                                                                                                                                                          406
                                                                                                                                                                                                                                                                                                     466
                                                                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                                                                                526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                          임
                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                à
                                                                                                   g
                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285
                                                                                                                                                                                                                    313 ICCATTICCTTAAAAIGCIGCTIAGIAACTAACAGGACAIGATIAGAGAGATTITICACAA 372
                                                                                                                                                                                                                                                                                                   373 idairiticciaciciticidiididifaaaaccaiciricaaatgaataaaadaada 432
                                                                                                                                                                                                                                                                                                                                            497
                                                                                                                                                                                                                                                                                                                                                                              433 AAAAAAATCAGTCAAGTAGTTGCACAACATACTTGGAATCAATATTTTAA 492
                                                                                                                                                                                                                                                                                                                                                                                                                         557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                          AGGATATITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 317
                                                                                                                                253 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 312
                                                                                                                                                                                  TCCATITCCTIAAAAIGCIGCTIAGIAACIACAGGACAIGAITAGAGAGAITITICACAA 377
                                                                                                                                                                                                                                                                 437
                               CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AGAGGATATTTCAACAATACCAGCCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 CIGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 IGATITITICCIACICITICIGITIGADADACCATCITICAAAIGAAAAACAAAGA
                                                                                                                                                                                                                                                                                                                                          438 AAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATGTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine
for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.1%; Score 423.4; DB 14;
93.4%; Pred. No. 8.6e-87;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10/9-/54A

US-10/9-/54A

US-10/9-/54A

Deblication No. US2020164625A1

GENERAL INFORMATION:

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Molenar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bov.

TITLE OF INVENTION: Mammary Gland and Methods for FILE REFERENCE: 11000-1068

CURRENT FILING DATE: 2002-02-19

PRIOR PILING DATE: 2000-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR PELICATION NUMBER: US 60,162,701

PRIOR PELING DATE: 2000-08-22

PRIOR PELING DATE: 2000-08-22

PRIOR PELING DATE: 2000-08-22

PRIOR PILING DATE: 2000-08-22

PRIOR PELING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOCTWARE: FASTESEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 TTACCATGCATGCTTAATAAATTGATCTATCAA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-079-754A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
                                                                                                                258
                                                                                                                                                                                         318
                                   198
                                                                        193
```

d

ò

g à В à

ð

```
US-09-992-600A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-079-754A-5
SEQ ID NO 3
LENGTH: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                     208 TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 cárgárrágágcrgárrcárcrgáagagágáaággcacaggaaágggaaaaaacarcarag 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTCACAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 ICCATITICCITAAAATGCTGCTTAGTAACTACAGGACATGATTAGGAGATTTTTCACAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AGGATATITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 CTGGACTCCACCAATATGAAGATCTTTATCTTTGTCTTGATTATGGCTCTCATCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 CAGGACTCCACCACAATATGAAGATCTTTATCTTTGTTCTTCATTATGGCTCTCACTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                                                                                                                    Sequence 200. Application US/10079623
Publication No. US20020169302A1
GENERAL INFORMATION:
APPLICANT: Harukkala, Ilkka J.
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: mammary gland and methods for their use.
FILE REPRENCE: 11000.104443
CURRENT FILICATION NUMBER: US/10/079,623
CURRENT FILICATION NUMBER: US/10/079,623
CURRENT FILICATION WARES: TOS. 2002-02-19
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10079754A
Publication No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenar, Adrian J.
FILE REFERENCE: 11000.1068
CURRENT FILING DATE: 2002-02-19
FRIOR APPLICATION NUMBER: US 09/694,190
FRIOR FILING DATE: 1999-10-29
FRIOR FILING DATE: 1999-10-29
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1990-08-22
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1990-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.5%; Score 238.4; DB 14; Length 267; Best Local Similarity 99.6%; Pred. No. 1.2e-44; Matches 239; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Bovine
                                                                                                                                                                                                                RESULT 6
US-10-079-623-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-623-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 200
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                            ò
```

```
ö
                                                                                                                                                                                                                                                                                             se caegacrocaccaaarargaagarcrirarcrirarcrircarrargecricicarccraec 115
                                                                                                                                                                                                                                                                                                                                                                                                           116 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGAGAAAAACGTCACAGGAAAAACGTCATGT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 TITCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTT 324
                                                                                                                                                                                                                                                                                                                                                      1 rircaacaaraccagccarargaacgararccacraaarrarcrccrccrgcgrarccarra 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Gridor, Matthew
APPLICANT: Gridor, Marthew
APPLICANT: Gridor, Marray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Momber: 1000.1068
CURRENT APPLICATION NUMBER: US 09/699,146
PRIOR PELLING DATE: 2000-10-27
PRIOR PELLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                  Length 869;
                                                                                                              Query Match
19.0%; Score 115; DB 14; Length 86
Best Local Similarity 92.4%; Pred. No. 3.3e-16;
Matches 121; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 14.4%; Score 87; DB 14; Length 96; Similarity 94.7%; Pred. No. 2.8e-10; 90; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 CCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTAAAATGCTGCTTACCAACTACAGGACATGAT 95
                                                                                                                                                                                                                                             138 CTGGACTCCACCAAATATGAAGATCTTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09992600A, Publication No. US20030027161A1, GENERAL INFORMATION: Stephane APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AGGATATTTTC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 ATGTATTCCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
TYPE: DNA
CRGANISM: Bovine
US-10-079-754A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Bovine
```

```
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 5
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09992095B Publication No. US20030157485A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.9%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-0
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                    LOCATION: 318..438
NAME/KEY: polyA_si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 84..317
                                                                                                                                                                        FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
NAME/KEY: CDS
LOCATION: 84..31'
NAME/KEY: 3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: JPatent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-992-095B-5
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-924-340-5
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGTA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GAATTICATCITICATGACTGGACTCCACCAAATATGGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GACTICTICTICAGIAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERRNCE: 91.US2.RSG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILMG DATE: 2001-08-06
PRIOR PELING DATE: 2001-08-06
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-15
        TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.4; DB 10; Length Pred. No. 3.6e-06; Mismatches 41; Indels
                      TILLE REPERENCE: 91.034.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 5
LIBNGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09924340 Publication No. US20030027248A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.9%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: polyA_signal
LOCATION: 397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: polyA site
, LOCATION: 423..438
US-09-992-600A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: 3'UTR
LOCATION: 318..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 84..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-924-340-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 cricacicicarantricarantriagoscreatricacarananalasacarcarasta 169
                                                                                                                                                                                                                                                                                                                                                                                             120 GAATTICATCITICAIGACTGGACTCCACCAAATAIGAAGAICTTTAICTTIGICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       so dacrerecterragagrada a de de contra de de contracter de
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILTE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILTE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILT APPLICATION NUMBER: US/09/992,095B
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
                                                                                                                                                                                              .
0
Length 438;
Score 70.4; DB 10; Length
Pred. No. 3.6e-06;
0; Mismatches 41; Indels
```

Gaps

```
110 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GAATITCAICITICAIGACTGGACTCCACCAAATATGAAGATCTTTATCTTGTCTTTGTCTTTGTT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGGT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TATGGCTCTCCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA 239
                                                                                                                                        120 GAATTICATCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                           50 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benjailow: Stephane
APPLICANT: Tanaka, Hiroaki
ITILEO PO INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERRICE: 91.086.DIV
CURRENT FILING DATE: 2001.11.14
PRIOR PILING DATE: 2001.01.11.4
PRIOR PLING DATE: 2001.08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PLING DATE: 2001.06-15
                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 70.4; DB 15; Length 438; Larity 69.9%; Pred. No. 3.6e-06; Conservative 0; Mismatches 41; Indels 0
         Query Match
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-000-489-5; Application US/10000489; Sequence 5; Application No. US20030092011A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 ACGGAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                       240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | LOCATION: 1..83
| NAME/KRY: CDS
| LOCATION: 84..31
| LOCATION: 384..31
| LOCATION: 318..438
| NAME/KRY: polyA signal
| LOCATION: 397..402
| NAME/KRY: polyA signal
| LOCATION: 423..438
| US-10-000-489-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 95,
                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTGCTTTAGT 109
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091USOBDIV
CURRENT FILING DATE: 2001-06-14
FRICH APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-05
PRIOR PLING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09999570 Publication No. US20030170628A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 ACGGAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 TAGAAGAAATTCCAT 185
                                                                                                                 NAME/KEY: polyA signal LOCATION: 397..402
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: polya_signal
LOCATION: 397..402
                                                                                                                                                                                                        // NAME/KEY: polyA_site
// LOCATION: 423..438
US-09-992-095B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY: polyA site
; LOCATION: 423..438
US-09-999-570-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 3'UTR
LOCATION: 318..438
                                                          318..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-999-570-5
                         NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

Gaps

2

```
Search completed: August 16, 2004, 00:23:18 Job time : 391 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TATGGCTCTCCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 crideicrichicarurciargarraececrearricacareaaaagacarcareera 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTALIUN: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.092.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT APPLICATION NUMBER: US/924,340
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/296,698
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10154678
Publication No. US20030162186A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hircaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182.US1.REG
CURRENT APPLICATION NUMBER: US/10/154,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70.4; DB 15;
Pred. No. 3.6e-06;
0; Mismatches 41;
                                                                                                                                 Sequence 5, Application US/1000986 Publication No. US20030096247A1 GENERAL INFORMATION:
170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.9%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 318..438
NAME/KEY: polyA signal
LOCATION: 397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: polya site LOCATION: 423..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 5'UTR
LOCATION: 1..83
NAME/KEY: CDS
LOCATION: 84..317
NAME/KEY: 3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-154-678-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-000-986-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

```
50 GACTCTCCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 criegerichearentecargarrageerigarreacargaaaagagareargera 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GAATTICATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 70.4; DB 15;
69.9%; Pred. No. 3.6e-06;
tive 0; Mismatches 41;
CURRENT FILING DATE: 2002-10-15
PRICR APPLICATION NUMBER: US 09/924,340
PRICR FILING DATE: 2001-08-06
PRICR FILING DATE: 2001-08-06
PRICR FILING DATE: 2001-07-13
PRICR FILING DATE: 2001-07-13
PRICR APPLICATION NUMBER: US 60/202,277
PRICR PILING DATE: 2001-06-15
PRICR PILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
SSOFTWARE: UP at ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 ACGGAAAAAACATCAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 TAGAAGAAATTCCAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.9
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: polyA_signal
LOCATION: 397..402
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: polyA site
LOCATION: 423..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 318..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 84..317
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: 5'UTR
LOCATION: 1..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: 3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-154-678-5
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
```

CB984475 AGENCOURT CB98521 AGENCOURT CB987745 AGENCOURT BX485825 DKFZD686L BX485714 DKFZD686E CB987175 AGENCOURT

EST89157 EST95743 EST89161 EST89145 2 BX283872

AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT

AGENCOURT AGENCOURT AGENCOURT

AGENCOURT AGENCOURT AGENCOURT

AAA3376700 BAA33782804 BBS AAA382804 BBS AAA

AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOURT AGENCOUR AGENCOURT

Perfect score:

Sequence:

OM nucleic

о ::

Run

Scoring table:

Searched:

Database

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Mammalia; Euteleostomi; Hominidae; Homo.

I (bases I to 553)

I (bases I to 553)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits cDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: NDCM443 row: b column: 08

High quality sequence stop: 553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB985810 553 bp mRNA linear EST 01-MAY-2003 AGENCOURT 13647469 NIH MGC 184 Homo sapiens cDNA clone IMAGE:30329983 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
CB984475
CB985521
CB987745
BX485825
                                                                    BX485714
CB987175
AA376700
AA382524
AA376704
AA376689
BX283872
                                                                                                                                                                                       CB986478
CB985159
CB985183
CB98523
CB98523
CB98523
CB985223
CB985223
CB958245
CB958245
CB958245
                                                                                                                                                                                                                                                                                                                                                                                   CB957121
CB957972
CB985184
                                                                                                                                                                                                                                                                                                                                                                                                                                     CB986281
CB986417
CB987123
CB987595
CB955720
CB956487
CB956860
CB956860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB985810.1 GI:30280334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB985810
78.6
778.6
77.6
77.6
77.6
                                                                                                                                         LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
CB985810
 CB985810 AGENCOURT
CB957544 AGENCOURT
CB986888 AGENCOURT
CB958289 AGENCOURT
                                                                                                               August 15, 2004, 07:37:23 ; Search time 2272 Seconds (without alignments) 7938.713 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                        604
1 gaagtattttcagttctata.......tatcaagcataaaaaaaa 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                    55026578
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                               nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB985810
CB957544
CB986888
CB958289
                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_estin...
em_estin...
em_estin...
em_estin...
em_estin...
em_estin...
gb_esti...
gb_esti...
gb_esti...
gb_esti...
gb_esti...
em_estin...
em_gss_hum...
em_gss_has...
em_gss_hum...
em_gss_has...
em_
                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                       US-10-079-754A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_estba:*
em_esthum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           estba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555
555
792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6
13.0
13.0
```

82.2 78.6 78.6 78.6

Score

Result Š. organism="Homo sapiens"

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                   /db_kxer="TRAGE:302993"
/lab_host="NAMGE:302993"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 184"
/clone lib="NIH MGC 184"
/clone lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc), Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned, cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC.3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCGCACATG-GT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contendined inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov

These Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be thrus, //image.llnigov

http://image.llnigov

I column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 29-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGGCA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 TGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAAACGGGAAAAAAACATCATAGAG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 TGATTGGAGCTGATTCATCTGAAGAGAATTTTTGCGTAGAATTGGAAGATTCGGTTATG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATAITITCAACAATACCAGCCATAICAACGAIAICCACTAAAITAICCTCCTGCGTAIC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GGTA---TGGCCCTTATCAGCCAGTTCCAGAACAACCACTATACCCACAACCATACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATCTTGGCTCTCATGGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

11 (bases 1 to 546)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 CATTICCTTAAAAIGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AATATACCTTTTAATATCACTCACAGGACATGATTATTGAGGCTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%; Score 82.2; DB 14; Length 553; 62.8%; Pred. No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB957544 13785762 NIH MGC_184 Homo sapiens CDNA clone
IMAGE:30352504 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 546.
Location/Qualifiers
                                                                              Ltype="mRNA"
xref="taxon:9606"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB957544.1 GI:30213661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB957544
                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB957544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imago.llnl.gov

Plate: NDCM141 row: k column: 23

High quality sequence stop: 551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GAATITCAICITTCAIGACTGGACTCCACCAATAIGAAGAICTTTAICTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTCTTTGTTTTGCTTTAGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTTATGG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 78.6; DB 14; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB986888 AGENCOURT 13650592 NIH MGC_184 Homo sapiens cDNA clone IMAGE:30329446 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.2%; Pred. No. 0.00
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB986888.1 GI:30281408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 TATAGAGGTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
CB986888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

```
CA). Note: this is a NIH MGC Library."
          60
                                                                                                                                     organism="Homo sapiens"
Plate: NDCMlbv .c... High quality sequence stop: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB984475.1 GI:30278999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 raradaggrir 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi:
Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
CB984475
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                  /Unit type="mRNA" | Modern the properties | Modern the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Charges I to 722.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB958289 792 bp mRNA linear EST 29-APR-2003
AGENCOURT_13778124 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30352112 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATITICATCITITICATGACTICCACCAAATATGAAGATCITITATCITIGICTTICAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TATGCCTCTCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GGACTATGGACCAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 78.6; DB 14; Length 555; 60.2%; Pred. No. 0.0016; ive 0; Mismatches 94; Indels 6.
                                                                    organism="Homo sapiens"
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB958289
CB958289.1 GI:30214405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 TATAGAGGTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB958289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

ORIGIN

g

ò

g

ò

g

 δ

Š

```
/MOL type="mRNA"
// Also Lype="mRNA"
// Also Lype="mRNA"
// Clone="INMENSISSI12"
// Alb host="DH10B (T1 phage-resistant)"
// Alb host="DH10B (T1 phage-resistant)"
// Lib host="DH10B (T1 phage-resistant)"
// Alb host="DH10B (T1 phage-resistant) |
// Alp host="DH10B (T1 phage-resistant) |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 radaadaaaarrecardaaaaa----carcarreacarcdadaarrrecarritares 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGGCATGAT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 793)

NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 cacricricrirgagraaaagacricagccaacrargaagrirrrrrrrrgcrirragr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution. MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT 13459298 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30327061 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 78.6; DB 14; Length 792; 60.2%; Pred. No. 0.0014; ive 0; Mismatches 94; Indels 6.
```

ä

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB987745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                 /dD.xtel="Taxon:9800"
/clone="IMAGE:3027061"
/lab host="NBLOB (TI phage-resistant)"
/clone="Organ: Poloid-diamodiar; Vector: pDNR-LIB; Site_1:
/clone="Organ: Poloid-diamodiar; Vector: pDNR-LIB; Site_1:
/clone="Organ: Poloid-diamodiar" (ggc.gcctcggcc);
Library is oligo-dT primed and directionally cloned, cDNR
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTRAAGGCGGAGGCGCATATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTRAAGGCGGGCGCGATATGGTG-dT(3)BN-3' (where B = A,
C' or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was emitched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDN Library Preparation: CLOWIECH Laboratories, Inc.
CDNA Library Arrayed Dy: The I.M.A.G.B. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TAGAAGAAAATTCCAT----GAAAAGCATCATTCACATCCAGAATTTCCATTTATGG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 13.0%; Score 78.6; DB 14; Length 793; al Similarity 60.2%; Pred. No. 0.0014; 151; Conservative 0; Mismatches 94; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB985521
AGENCOURT 13652179 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30327553 5', mRNA sequence.
found through the I.M.A.G.E. Consortium/LLNL at:
                       http://image.llnl.gov
Plate: NDCM135 row: h column: 14
High quality sequence srop: 486.
Location/Qualifiers
                                                                                                                                                             'organism="Homo sapiens"
                                                                                                                                                                                             mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB985521.1 GI:30280045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 TATAGAGGTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
CB985521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
```

ઠે g à d ò qq δ g à

```
/OLGITANGE SEPTERS //OLGITANGE SEPTERS //OLGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB987745
AGENCOURT 13621497 NIH MGC 184 Homo sapiens cDNA clone
MAGE:30327757 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 GACTOTÓCTOTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NCGMS row: m column: 02
High quality sequence stop: 177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 TAGAAGAAACTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GAATTICATCITICATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%; Score 78.6; DB 14; Length 831; 60.2%; Pred. No. 0.0013; tive 0; Mismatches 94; Indels 6;
DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB987745.1 GI:30282265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 TAGAGAGATIT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 ratadadgrir 285
                                                                                                                                                                                                                                                                                                                                                                                                 .831
```

```
BX485714 622 bp mRNA linear EST 04-SEP-2003 DKFZp686EE20248 rl 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686EE20248 5', mRNA sequence.
                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AAAITAICCICCIGCGIAICCATIICCITAAAAIGCIGCITAGIAACIACAGGACAIGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 TATAGAG--GTAAGCTGACTCTAGTTGCTTGTCTTTCTAGAAGTGTCACACACTGACAGTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 622)

Ottenwaelder, D., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hlcc3)"
Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                   This clone (DKPZp686L09248) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 TAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGAAAACCATCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GAATTTCATCTTTCATGACTGGACTCCACAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 gacricricrirgagraaaaggacricagccaacrargaagrrirrirgrirrirgcrriragr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TAIGGCICTCATCCTAGCCAIGATTAGAGCIGATICATCTGAAGAGAAACGICACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 77.6; DB 13;
Similarity 56.2%; Pred. No. 0.0023;
19; Conservative 0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 AAATGAATAAAACAAAGAAAAAAAAAATCAGTCAAGT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 TAAAAAAAAGCCATAAGCTAACAACCATTCCAGT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="686 (synonym:
/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686L09248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX485714.1 GI:31948727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              et al.)
Unpublished (2003)
                                          Contact: MIPS
MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX485714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Simenes 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
BX485714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                          High quality sequence stops: 386.

Location/Qualifiers

1.929

Location/Qualifiers

1.929

Anol_type="mRNa" "Homo sapiens"

| Mol_type="mRNa" | Homo sapiens | Mol_type="mRNa" | Homo sapiens | Mol_type="mRNa" | Homo sapiens | Mol_type="mRNa" | Homo sapiens | Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear CST 04-SEP-2003 hlcc3) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
Meil,B., Amid,C., Osanger,A., Robo,G., Han,M. and Wiemann,S.
EST (Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
et al.)
                                                                                                         pe
p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 criegicicicarcarricardarragecercarreargaaaagagaareargaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Plate: NpCM137 row: e column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78.6; DB 14;
Pred. No. 0.0013;
0; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 bp
DKFZp686L09248 r1 686 (synonym: i
DKFZp686L09248 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX485825.1 GI:31948944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
llarity 60.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATAGAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
BX485825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
```

g

ò

g

ò

셤

ò

g

8

179

ώ ώ

97

239

211

419

271

```
AA376700
AA376700.1 GI:2029018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch
il Similarity 59.8%;
150; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 TATAGAGGTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
AA376700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DREZ); Bmiss wiemanngdkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TATGGCTCTCATCCTAGCCAȚGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 IAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGAAAACCATCTTTC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 TATAGAG--GTAAGCTGACTCTAGTTACTTGTCTTTGTAGAAGTGTCAACACTGACAGTT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 773)

                                                                                                                                                                                                                                                                                                                                                                                                                                                              hlcc3)"
Site_1: SfiIA; Site_2: SfilB;
                                                                                                                                                                                                     This clone (DKFZp686E20248) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB987175 773 bp mRNA linear EST
AGENCOURT 13650773 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:33329891 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%; Score 77.6; DB 13; Length 622; 56.2%; Pred. No. 0.0023; ive 0; Mismatches 139; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 AAATGAATAAACAAAGAAAAAAAATCAGTCAAGT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 TAAAAAAAAAGCCATAAGCTAACAACCATTCCAGT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="686 (synonym:
/note="Vector: pTriplEx2;
                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686E20248"
                                                                                                                                                                                                                                                                                                                                                                                                             'dev_stage="adult"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB987175.1 GI:30281695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 189; Conservative
                                                                                                                                                                                                                                                                                                     . 622
  Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB987175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
CB987175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

ઠે d δ g ò 임 ò g à g à

```
AA376700 312 bp mRNA linear EST 21-APR-1997 EST89157 Salivary gland Homo sapiens CDNA 5' end similar to histatin 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1 (Dases 1 to 312)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, B.F., Weinstrock, K.G., Goosyne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, I.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTTGAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTÄTGAAGTTTTTTGTCTTTGCTTTAGT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 TAGAAGAAATTCCAT----GANAAGCATCATTCACATCGAGAATTTCCATTTTATGG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 274
cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution. MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77.6; DB 14; Length 773; Pred. No. 0.002; 0; Mismatches 95; Indels 6;
                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDCM142 row: n column: 12
                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                        High quality sequence stop: 181.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
```

```
AA382524.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                      REFERENCE
AUTHORS
      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, F.S.T., Kelley, J.M., Kelley, J.M., Kelley, J.M., Merrick, J.M., Kelley, J.M., Kelley, J.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Merrick, J.M., Moreno-Palanques, R.E., Scott, J.L., Saudek, D.M., Shritey, R.S., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., M. Dinke, D.F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Frankon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Frankon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTTATGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /.organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):181117"
/db_xref="Haxon:9606"
/dev_stage="adult"
/clone_lib="salivary gland"
/nore="Organ: salivary gland, Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 crigecicicargarirecargariragecrigaricaeargaaagagacarcargegra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GAAFTFCAFCTFFCAFGACTGGACTCCACCAAATATGAAGAFCTFFAFCFFFGFCFFCAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 77; DB 9; Length 312; 59.8%; Pred. No. 0.004; ive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTS: EST89156 THC102726
Contact: Kerlavage, AR
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.7
Best Local Similarity 59.8
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAGAGGTTT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
AA382524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

EST 21-APR-1997

AA382524
327 bp mRNA linear EST 21-APR-199
SET95743 Testis I Homo sapiens CDNA 5' end similar to histatin 1,
mRNA sequence.
AA382524

DEFINITION

ACCESSION

```
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 cricácricicargariticcargaritagcecricaricacargaaaagagacarcargegra 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 geacriarggarczaarriarcrarargacaarrgararccriagraarcargegegerargar 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/clonellib="restis I"
/note="organ: testis; Vector: pBluescript SK-; Site_1:
// Scori; Site_2: Xho!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTGCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TATGGCTCTCCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="ATCC (inhost):186803"
/db_xref="taxon:9606"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 77; DB 9;
llarity 59.8%; Pred. No. 0.0039;
Conservative 0; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other ESTs: THC102726
Contact: Kerlavage, AR
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

8 g

```
Homo saptens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

To (bases 1 to 348)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Mite, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlon, E., Hinkle, P.S., T.,

Kelley, J.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisens, S.M.,

Rymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Rashings, G.A.,

Rymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Rashings, S., Olsen, H.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisens, S.M.,

Billion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA376689 348 bp mRNA linear EST 21-APR-1997 EST69145 Salivary gland Homo sapiens CDNA 5' end similar to histotin 1, mRNA sequence.
                                                  76 circaccicicargarinceargariagececrearicacargaaaagacarearga 135
                                                                                                          240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                      136 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTTATGG 189
                                                                                                                                                                                                                                 300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                       190 ggacrarggarcaagraricrarargacaarrgararccrragraarcargggggargar 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mo! type="mgXX(in")
/db xref="xaxCX(inhost):181112"
/db xref="taxon:9606"
/db xref="adult"
/dev stage="adult"
/clone lib="Salivary gland"
/note="Organ: salivary gland; Vector: pBluescript SK-;
180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other ESTs: EST89144 THC102726
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA376689.1 GI:2029007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                            360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                    250 raradaddrir 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA376689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
AA376689
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                              ద
                                                                                                                                                                               엄
                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Te (bases 1 to 330)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Ghehr, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.W.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Kyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Dinke, D.P., Feng, D.F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J.C., Li, H., Meissner, P.S., Olsen, H.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                           330 bp mRNA linear EST 21-APR-1997
EST89161 Salivary gland Homo sapiens CDNA 5' end similar to
halfatin 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GAATITCAICITICAIGACIGGACICCACCAAAIAIGAAGAICTITAICITIGICITICAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/clond lib="salivary gland"
/note="Organ: salivary gland; Vector: pBluescript SK-;
Site_1: Ecox1; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATC" (inhost):181119"
/db_xref="taxon:9606"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 77; DB 9;
1larity 59.8%; Pred. No. 0.0038;
Conservative 0; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other ESTS: EST89160 THC102726
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     AA376704.1 GI:2029022
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                       258 TATAGAGGITT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
                                                  360 TAGAGAGATIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 150; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7566098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBMED
                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURES
                                                                                                                                                                                                                              AA376704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
```

ð g

ਨੇ 셤 8 셤 ò g ð g ò g

```
360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Job time : 2275 secs
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX283872 NIH_MGC_81 Homo sapiens cDNA clone IMAGp958N191131 ;
IMAGE:4289874, mRNA sequence.
                                                                                                                                                                                                                                                                120 GAATTICATCITICAIGACIGGACICCACCAAAIAIGAAGAICITIAICTITIGICTICAI 179
                                                                                                                                                                                                                                                                                                                                                                                                                       180 TATGGCTCTCTCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TAGAAGAAATTCCAT----GAAAGCATCATTCACATCGAGAATTTCCATTTTATGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 GGACTATGGATCAAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mcMa" or proceed that the process of the proceed of the process of the
                                                                                                                                                                                                                                                                                                                                              GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTGGT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (200 390)

1 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human Unigenesset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer:
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RZPD Deutsches Resourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD, INAGPSSRN191131.
RZPDLIB! I.M.A.G.E. CDNA CLONE COllection; Human UnigeneSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response71sNcgi-bin/showlib.pl.cgi/response71sNcgi-bin/showlib.pl.cgi/response71sNcgi-Britany GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: 449 30 32639 101
Fax: 449 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free from RZPD; contact RZPD (clonearzpd.de) for further information. Seq pCWV-M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT. Location/Qualifiers
                                                                                                                                                                                               . 9
                                                                                                                  Length 348;
                                                                         Score 77; DB 9; Length 2x., Pred. No. 0.0038;
Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX283872.1 GI:28848326
EST.
                                                                                                              12.7%;
59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAGAGGTTT 256
                                                                                                 Query Match
Best Local Similarity
Matches 150; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX283872
                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
BX283872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                ORIGIN
```

```
and 3' adaptor sequence:

'A-ATTCTAGAGGGGGGGGGGACATG-dT(30)BN-3' (where B = A, C, ATTCTAGAGGGGGGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo, Alto, CA)."
```

Gaps . 9 Score 77; DB 13; Length 390; Pred. No. 0.0036; 0; Mismatches 95; Indels 12.7%; 59.8%; Best Local Similarity 59.8 Matches 150; Conservative

ij,

300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359

269 TATAGAGGTTT 279

Search completed: August 16, 2004, 00:15:22

Lhis Page Blank (uspto)